```
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 13 AA;

Query Match             90.3%;  Score 65;  DB 4;  Length 13;
Best Local Similarity   84.6%;  Pred. No. 0.00033;
Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 CASELGKSTNTFC 13
                |||||||:||||
Db            1 CASELGKTSNTFC 13


RESULT 7
AAU04537
ID   AAU04537 standard; peptide; 13 AA.
XX
AC   AAU04537;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based monocyclic peptide 15.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  1..13
FT                   /note= "This bond cyclises the peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 25; Page 47; 102pp; English.
XX
CC   The sequence represents a monomeric monocyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 13 AA;

Query Match             90.3%;  Score 65;  DB 4;  Length 13;
Best Local Similarity   84.6%;  Pred. No. 0.00033;
Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 CASELGKSTNTFC 13
                |||||||:|||:||
Db            1 CASELGRSTNSFC 13


RESULT 8
AAU04547
ID   AAU04547 standard; peptide; 17 AA.
XX
AC   AAU04547;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #4.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  1..13
FT                   /note= "This bond cyclises the peptide"
FT   Disulfide-bond  17
FT                   /note= "A disulfide bond forms between residue 17 and
FT                   residue 17 of an identical peptide to form a dimeric
FT                   peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
```

```
PS    Example 26; Page 49; 102pp; English.
XX
CC    The sequence represents a dimeric bicyclic peptide of the invention,
CC    whose 3-dimensional structure is modelled on the expose loop of human
CC    VEGFD (vascular endothelial growth factor). The invention relates to a
CC    method of producing a monomeric monocyclic peptide by a measuring beta-
CC    beta carbon separation distances on opposite antiparallel strands of a
CC    peptide loop fragment from an exposed loop of a growth factor protein and
CC    cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC    peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC    peptides) and a cyclic peptide with at least one amino acid deleted prior
CC    to cyclisation are used to interfere with angiogenesis,
CC    neovascularisation or lymphangiogenesis in a mammal with a condition
CC    characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC    The condition is diabetic retinopathy, psoriasis, arthropathy,
CC    hemangioma, vascularised malignant or benign tumour, post-recovery
CC    cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC    trauma, substance-induced neovascularisation of the liver, excessive
CC    hormone-related angiogenic dysfunction, diabetes induced neovascular
CC    sequelae, hypertension induced neovascular sequelae, or chronic liver
CC    infection. The peptides are also used to modulate vascular permeability
CC    in a mammal (the mammal has a condition characterised by fluid
CC    accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC    or brain. The peptides are used to image blood vessels and lymphatic
CC    vasculature. The monomeric and bicyclic peptides are used to interfere
CC    with at least one biological activity induced by VEGF, VEGF-C or -D and
CC    are also used in combination with an anti-inflammatory agent, to treat a
CC    chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC    diabetic retinopathy
XX
SQ    Sequence 17 AA;

Query Match     90.3%;   Score 65;  DB 4;  Length 17;
Best Local Similarity  84.6%;   Pred. No. 0.00044;
Matches  11;  Conservative  2;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 CASELGKSTNTFC 13
         |||||:||||:||||
Db     1 CASELGKTSNTFC 13

RESULT 9
AAU04551
ID   AAU04551 standard; peptide; 17 AA.
XX
AC   AAU04551;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #8.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Disulfide-bond  1..13
FT                  /note= "This bond cyclises the peptide"
FT   Disulfide-bond  17
FT                  /note= "A disulfide bond forms between residue 17 and
FT                  residue 1 of the sequence appearing as AAU04528, forming
FT                  a dimeric peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
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PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 26; Page 49; 102pp; English.
XX
CC   The sequence represents a dimeric bicyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 17 AA;

Query Match     90.3%;   Score 65;  DB 4;  Length 17;
Best Local Similarity  84.6%;   Pred. No. 0.00044;
Matches  11;  Conservative  2;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 CASELGKSTNTFC 13
         |||||:|||:||||
Db     1 CASELGRSTNSFC 13

RESULT 10
AAU04549
ID   AAU04549 standard; peptide; 17 AA.
XX
AC   AAU04549;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #6.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Disulfide-bond  1..13
```

FT   Disulfide-bond   /note= "This bond cyclises the peptide"
FT   17
FT   /note= "A disulfide bond forms between residue 17 and
FT   residue 17 of an identical peptide to form a dimeric
FT   peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-44248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 26; Page 49; 102pp; English.
XX
CC   The sequence represents a dimeric bicyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 17 AA;

Query Match   90.3%; Score 65; DB 4; Length 17;
Best Local Similarity   84.6%; Pred. No. 0.00044;
Matches   11; Conservative   2; Mismatches   2; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFC 13
              ||||||:||:||||
Db   1 CASELGRSTNSFC 13

DT   26-SEP-2001 (first entry)
XX
DE   VEGF based monocyclic peptide 14.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Disulfide-bond   1..13
FT   /note= "This bond cyclises the peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-44248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 25; Page 47; 102pp; English.
XX
CC   The sequence represents a monomeric monocyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 13 AA;

Query Match   84.7%; Score 61; DB 4; Length 13;
Best Local Similarity   76.9%; Pred. No. 0.0016;
Matches   10; Conservative   3; Mismatches   3; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFC 13
              |||::||||||:|

RESULT 11
AAU04536
ID   AAU04536 standard; peptide; 13 AA.
XX
AC   AAU04536;
XX

Qy   1 CASELGKSTNTFC 13
              |||::|||||||:|

Db   1 CASDVGKSTNTWC 13

RESULT 12
AAU04548
ID AAU04548 standard; peptide; 17 AA.
XX
AC AAU04548;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based bicyclic dimeric peptide #5.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT Disulfide-bond 1. .13
FT   /note= "This bond cyclises the peptide"
FT Disulfide-bond 17
FT   /note= "A disulfide bond forms between residue 17 and
FT   residue 17 of an identical peptide to form a dimeric
FT   peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Example 26; Page 49; 102pp; English.
XX
CC The sequence represents a dimeric bicyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGFD (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a
CC peptide loop fragment from an exposed loop of a growth factor protein and
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC peptides) and a cyclic peptide with at least one amino acid deleted prior
CC to cyclisation are used to interfere with angiogenesis,
CC neovascularisation or lymphangiogenesis in a mammal with a condition
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, neovascular... psoriasis; arthropathy;
CC hemangioma, vascularised malignant or benign tumour; post-recovery
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC trauma, substance-induced neovascularisation of the liver, excessive
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
CC sequelae, hypertension induced neovascular sequelae, or chronic liver
CC infection. The peptides are also used to modulate vascular permeability
CC in a mammal (the mammal has a condition characterised by fluid
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC or brain. The peptides are used to image blood vessels and lymphatic
CC vasculature. The monomeric and bicyclic peptides are used to interfere

CC with at least one biological activity induced by VEGF, VEGF-C or -D and
CC are also used in combination with an anti-inflammatory agent, to treat a
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC diabetic retinopathy
XX
SQ Sequence 17 AA;

Query Match   84.7%; Score 61; DB 4; Length 17;
Best Local Similarity 76.9%; Pred. No. 0.0021;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
        |||:||||||||:|
Db 1 CASDVGKSTNTWC 13

RESULT 13
AAU04522
ID AAU04522 standard; protein; 73 AA.
XX
AC AAU04522;
XX
DT 26-SEP-2001 (first entry)
XX
DE Human VEGF-D amino acids Val101-Thr 173.
XX
KW Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation.
XX
OS Homo sapiens.
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Example 1; Page 90-91; 102pp; English.
XX
CC The sequence represents Human VEGF-D (vascular endothelial growth factor)
CC amino acids Val101-Thr 173, used together with the C-terminal 23 residues
CC of VEGF to make a hybrid theoretical molecule for 3 dimensional
CC modelling. The sequence is used in a method of producing a monomeric
CC monocyclic peptide by a measuring beta-beta carbon separation distances
CC on opposite antiparallel strands of a peptide loop fragment from an
CC exposed loop of a growth factor protein and cyclising the peptide by
CC oxidising the cysteine residues. The monocyclic peptides, dimeric
CC bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
CC peptide with at least one amino acid deleted prior to cyclisation are
CC used to interfere with angiogenesis, neovascularisation or
CC lymphangiogenesis in a mammal with a condition characterised by
CC angiogenesis, neovascularisation or lymphangiogenesis. The condition is
CC diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
CC malignant or benign tumour, post-recovery cerebrovascular accident, post-
CC angioplasty restenosis, head, heat or cold trauma, substance-induced
CC neovascularisation of the liver, excessive hormone-related angiogenic
CC dysfunction, diabetes induced neovascular sequelae, hypertension induced

```
RESULT 14
AAU04520
ID   AAU04520 standard; protein; 96 AA.
XX
AC   AAU04520;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human VEGF-D amino acids Val101-PRO186.
XX
KW   Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 1; Page 89; 102pp; English.
XX
CC   The sequence represents Human VEGF-D (vascular endothelial growth factor)
CC   amino acids Val101-PRO186. The sequence is used in a method of producing
CC   a monomeric monocyclic peptide by a measuring beta-beta carbon separation
CC   distances on opposite antiparallel strands of a peptide loop fragment
CC   from an exposed loop of a growth factor protein and cyclising the peptide
CC   by oxidising the cysteine residues. The monocyclic peptides, dimeric
CC   bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
CC   peptide with at least one amino acid deleted prior to cyclisation are
CC   used to interfere with angiogenesis, neovascularisation or
CC   lymphangiogenesis in a mammal with a condition characterised by
CC   angiogenesis, neovascularisation or lymphangiogenesis. The condition is
CC   diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
CC   malignant or benign tumour, post-recovery cerebrovascular accident, post-
CC   neovascular sequelae, or chronic liver infection. The peptides are also
CC   used to modulate vascular permeability in a mammal (the mammal has a
CC   condition characterised by fluid accumulation in peripheral limbs or in
CC   lungs, peritoneal cavity, pleura, or brain. The peptides are used to
CC   image blood vessels and lymphatic vasculature. The monomeric and bicyclic
CC   peptides are used to interfere with at least one biological activity
CC   induced by VEGF, VEGF-C or -D and are also used in combination with an
CC   anti-inflammatory agent, to treat a chronic inflammation, especially
CC   rheumatoid arthritis, psoriasis and diabetic retinopathy
XX
SQ   Sequence 73 AA;

Query Match             75.0%;  Score 54;  DB 4;  Length 73;
Best Local Similarity   100.0%;  Pred. No. 0.15;
Matches   11;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          2 ASELGKSTNTF 12
              |||||||||||
Db         21 ASELGKSTNTF 31
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```
RESULT 15
AAY23889
ID   AAY23889 standard; protein; 109 AA.
XX
AC   AAY23889;
XX
DT   21-SEP-1999  (first entry)
XX
DE   Human vascular endothelial growth factor (VEGF)-D.
XX
KW   Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma;
KW   tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft;
KW   wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.
XX
OS   Homo sapiens.
XX
PN   WO9933485-A1.
XX
PD   08-JUL-1999.
XX
PF   23-DEC-1998;   98WO-US027373.
XX
PR   24-DEC-1997;   97AU-00001131.
PR   29-MAY-1998;   98US-0087392P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Stacker SA, Alitalo K;
XX
DR   WPI; 1999-405368/34.
XX
PT   A human cell line stably expressing vascular endothelial growth factor D,
PT   useful for treating melanomas or tumors expressing VEGF-D.
XX
PS   Claim 6; Page 72; 79pp; English.
XX
CC   The present sequence represents human vascular endothelial growth factor
CC   (VEGF)-D. The specification describes a human cell line which stably
CC   expresses VEGF-D, or fragments/analogues having VEGF-D biological
CC   activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex
CC   DNA, VEGF-D variants or antibodies (especially chimeric antibodies), are
CC   useful for the treatment or alleviation of malignant melanomas, tumours
CC   or psoriasis. Angiogenesis and lymphangiogenesis stimulating amounts of
CC   VEGF-D can be administered to enhance the acceptance and/or healing of
CC   skin grafts or to stimulate the healing of a surgical or traumatic wound
CC   to the skin. Lymphangiogenesis stimulating amounts of VEGF-D can be used
CC   to treat lymphedema. Endothelial proliferation stimulating amounts of
CC   VEGF-D are used to treat scleroderma. Vascularisation stimulating amounts
CC   of VEGF-D can be used to treat anhydrotic ectodermal dysplasia. VEGF-D
CC   angioplasty restenosis, head, heat or cold trauma, substance-induced
CC   neovascularisation of the liver, excessive hormone-related angiogenic
CC   dysfunction, diabetes induced neovascular sequelae, hypertension induced
CC   neovascular sequelae, or chronic liver infection. The peptides are also
CC   used to modulate vascular permeability in a mammal (the mammal has a
CC   condition characterised by fluid accumulation in peripheral limbs or in
CC   lungs, peritoneal cavity, pleura, or brain. The peptides are used to
CC   image blood vessels and lymphatic vasculature. The monomeric and bicyclic
CC   peptides are used to interfere with at least one biological activity
CC   induced by VEGF, VEGF-C or -D and are also used in combination with an
CC   anti-inflammatory agent, to treat a chronic inflammation, especially
CC   rheumatoid arthritis, psoriasis and diabetic retinopathy.
XX
SQ   Sequence 96 AA;

Query Match             75.0%;  Score 54;  DB 4;  Length 96;
Best Local Similarity   100.0%;  Pred. No. 0.2;
Matches   11;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          2 ASELGKSTNTF 12
              |||||||||||
Db         21 ASELGKSTNTF 31
```

CC   antibodies are useful for detecting tumours expressing VEGF-D. Fully-
CC   processed VEGF-D can be used to stimulate at least one VEGF-D bioactivity
CC   chosen from endothelial cell proliferation, migration, survival and
CC   differentiation and lymphangiogenesis without inducing vascular
CC   permeability
XX
SQ   Sequence 109 AA;

Query Match   75.0%; Score 54; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ASELGKSTNTF 12
           |||||||||||
Db   29 ASELGKSTNTF 39

Search completed: September 5, 2004, 09:55:09
Job time : 43.6768 secs

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          GenCore version 5.1.6

     Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    September  5, 2004, 10:00:15 ; Search time 36.5051 Seconds
                                        (without alignments)
                                        112.199 Million cell updates/sec

Title:          US-09-761-636A-5
Perfect score:  72
Sequence:       1 CASELGKSTNTFC 13

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters:    1298764

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  .Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	72	100.0	13	9	US-09-761-636A-5	Sequence 5, Appli
2	72	100.0	17	9	US-09-761-636A-8	Sequence 8, Appli
3	69	95.8	13	9	US-09-761-636A-15	Sequence 15, Appli
4	69	95.8	17	9	US-09-761-636A-27	Sequence 27, Appl
5	69	95.8	17	9	US-09-761-636A-31	Sequence 31, Appl
6	65	90.3	13	9	US-09-761-636A-16	Sequence 16, Appl
7	65	90.3	13	9	US-09-761-636A-18	Sequence 18, Appl
8	65	90.3	17	9	US-09-761-636A-28	Sequence 28, Appl
9	65	90.3	17	9	US-09-761-636A-30	Sequence 30, Appl
10	65	90.3	17	9	US-09-761-636A-32	Sequence 32, Appl
11	61	84.7	13	9	US-09-761-636A-29	Sequence 29, Appli
12	61	84.7	17	9	US-09-761-636A-3	Sequence 3, Appli
13	54	75.0	73	9	US-09-761-636A-1	Sequence 1, Appli
14	54	75.0	96	9	US-09-761-636A-1	Sequence 1, Appli
15	54	75.0	109	9	US-09-956-095-3	Sequence 3, Appli
16	54	75.0	109	9	US-09-219-345A-1	Sequence 1, Appli
17	54	75.0	109	16	US-10-779-731-1	Sequence 1, Appli
18	54	75.0	197	12	US-10-352-153-8	Sequence 8, Appli
19	54	75.0	280	13	US-10-044-622-1	Sequence 1, Appli
20	54	75.0	325	14	US-10-274-953-3	Sequence 3, Appli
21	54	75.0	325	14	US-10-161-694-3	Sequence 3, Appli
22	54	75.0	354	9	US-09-956-095-2	Sequence 2, Appli
23	54	75.0	354	9	US-09-219-345A-11	Sequence 11, Appl
24	54	75.0	354	9	US-09-795-006A-119	Sequence 119, App
25	54	75.0	354	10	US-09-375-248-6	Sequence 6, Appli
26	54	75.0	354	12	US-09-765-534B-22	Sequence 22, Appl
27	54	75.0	354	12	US-10-661-740-6	Sequence 6, Appli
28	54	75.0	354	14	US-10-262-538-26	Sequence 26, Appl
29	54	75.0	354	14	US-10-274-953-5	Sequence 5, Appli
30	54	75.0	354	14	US-10-161-694-5	Sequence 5, Appli
31	54	75.0	354	14	US-10-174-930-1	Sequence 1, Appli
32	54	75.0	362	13	US-10-139-876-4	Sequence 4, Appli
33	51	70.8	48	13	US-10-139-876-5	Sequence 5, Appli
34	51	70.8	81	13	US-10-086-623-18	Sequence 18, Appl
35	51	70.8	81	14	US-10-260-539-18	Sequence 18, Appl
36	51	70.8	110	10	US-09-847-524-6	Sequence 6, Appli
37	51	70.8	321	10	US-09-847-524-4	Sequence 4, Appli
38	51	70.8	321	14	US-10-274-953-9	Sequence 9, Appli
39	51	70.8	321	14	US-10-161-694-9	Sequence 9, Appli
40	51	70.8	358	9	US-09-852-209A-13	Sequence 13, Appl
41	51	70.8	358	10	US-09-847-524-2	Sequence 2, Appli
42	51	70.8	358	12	US-10-439-337A-13	Sequence 13, Appl
43	51	70.8	358	12	US-10-303-997B-13	Sequence 13, Appl
44	51	70.8	358	13	US-10-139-876-2	Sequence 2, Appli
45	51	70.8	358	14	US-10-131-600-13	Sequence 13, Appl

ALIGNMENTS

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RESULT 1
US-09-761-636A-5
; Sequence 5, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
;  APPLICANT: ACHEN, Marc
;  APPLICANT: STACKER, Steven
;  APPLICANT: HUGHES, Richard
;  APPLICANT: CENDRON, Angela
;  TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
;  FILE REFERENCE: 1064/48505 Achen et al
;  CURRENT APPLICATION NUMBER: US/09/761,636A
;  CURRENT FILING DATE: 2001-01-18
;  PRIOR APPLICATION NUMBER: US 60/176,293
;  PRIOR FILING DATE: 2000-01-18
;  PRIOR APPLICATION NUMBER: US 60/204,590
;  PRIOR FILING DATE: 2000-05-16
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: Patentin version 3.0
;  SEQ ID NO 5
;  LENGTH: 13
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-761-636A-5

  Query Match             100.0%;  Score 72;  DB 9;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-06;
  Matches   13;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CASELGKSTNTFC 13
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Db          1 CASELGKSTNTFC 13

RESULT 2
US-09-761-636A-8
; Sequence 8, Application US/09761636A
; Patent No. US20020065218A1
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GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-8

Query Match   100.0%; Score 72; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches   13; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFC 13
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Db   1 CASELGKSTNTFC 13

RESULT 3
US-09-761-636A-15
; Sequence 15, Application US/09761636A
; Patent No. US2002006521BA1
GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-15

Query Match   95.8%; Score 69; DB 9; Length 13;
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Matches   12; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFC 13
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Db   1 CATELGKSTNTFC 13

RESULT 4
US-09-761-636A-27
; Sequence 27, Application US/09761636A
; Patent No. US2002006521BA1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela

; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
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; SEQ ID NO 27
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; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-27

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Matches   12; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFC 13
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Db   1 CATELGKSTNTFC 13

RESULT 5
US-09-761-636A-31
; Sequence 31, Application US2002006521BA1
; Patent No. US2002006521BA1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-31

Query Match   95.8%; Score 69; DB 9; Length 17;
Best Local Similarity 92.3%; Pred. No. 3e-05;
Matches   12; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFC 13
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Db   1 CASELGKSTNTYC 13

RESULT 6
US-09-761-636A-16
; Sequence 16, Application US/09761636A
; Patent No. US2002006521BA1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293

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;   PRIOR FILING DATE: 2000-01-18
;   PRIOR APPLICATION NUMBER: US 60/204,590
;   PRIOR FILING DATE: 2000-05-16
;   NUMBER OF SEQ ID NOS: 34
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-16

Query Match           90.3%;  Score 65;  DB 9;  Length 13;
Best Local Similarity 84.6%;  Pred. No. 0.00011;
Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CASELGKSTNTFC 13
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Db          1 CASELGKTSNTFC 13


RESULT 7
US-09-761-636A-18
; Sequence 18, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
;   APPLICANT: ACHEN, Marc
;   APPLICANT: STACKER, Steven
;   APPLICANT: HUGHES, Richard
;   APPLICANT: CENDRON, Angela
;   TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
;   FILE REFERENCE: 1064/48505 Achen et al
;   CURRENT APPLICATION NUMBER: US/09/761,636A
;   CURRENT FILING DATE: 2001-01-18
;   PRIOR APPLICATION NUMBER: US 60/176,293
;   PRIOR FILING DATE: 2000-01-18
;   PRIOR APPLICATION NUMBER: US 60/204,590
;   PRIOR FILING DATE: 2000-05-16
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; ORGANISM: synthetic construct
US-09-761-636A-18

Query Match           90.3%;  Score 65;  DB 9;  Length 13;
Best Local Similarity 84.6%;  Pred. No. 0.00011;
Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CASELGKSTNTFC 13
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Db          1 CASELGRSTNSFC 13


RESULT 8
US-09-761-636A-28
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; Patent No. US20020065218A1
; GENERAL INFORMATION:
;   APPLICANT: ACHEN, Marc
;   APPLICANT: STACKER, Steven
;   APPLICANT: HUGHES, Richard
;   APPLICANT: CENDRON, Angela
;   TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
;   FILE REFERENCE: 1064/48505 Achen et al
;   CURRENT APPLICATION NUMBER: US/09/761,636A
;   CURRENT FILING DATE: 2001-01-18
;   PRIOR APPLICATION NUMBER: US 60/176,293
;   PRIOR FILING DATE: 2000-01-18
;   PRIOR APPLICATION NUMBER: US 60/204,590
;   PRIOR FILING DATE: 2000-05-16
;   NUMBER OF SEQ ID NOS: 34
;   SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 28
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-28

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Best Local Similarity 84.6%;  Pred. No. 0.00015;
Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CASELGKSTNTFC 13
              |||||||::||||
Db          1 CASELGKTSNTFC 13


RESULT 9
US-09-761-636A-30
; Sequence 30, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
;   APPLICANT: ACHEN, Marc
;   APPLICANT: STACKER, Steven
;   APPLICANT: HUGHES, Richard
;   APPLICANT: CENDRON, Angela
;   TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
;   FILE REFERENCE: 1064/48505 Achen et al
;   CURRENT APPLICATION NUMBER: US/09/761,636A
;   CURRENT FILING DATE: 2001-01-18
;   PRIOR APPLICATION NUMBER: US 60/176,293
;   PRIOR FILING DATE: 2000-01-18
;   PRIOR APPLICATION NUMBER: US 60/204,590
;   PRIOR FILING DATE: 2000-05-16
;   NUMBER OF SEQ ID NOS: 34
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-30

Query Match           90.3%;  Score 65;  DB 9;  Length 17;
Best Local Similarity 84.6%;  Pred. No. 0.00015;
Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CASELGKSTNTFC 13
              |||||||::||||
Db          1 CASELGKTSNTFC 13


RESULT 10
US-09-761-636A-32
; Sequence 32, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
;   APPLICANT: ACHEN, Marc
;   APPLICANT: STACKER, Steven
;   APPLICANT: HUGHES, Richard
;   APPLICANT: CENDRON, Angela
;   TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
;   FILE REFERENCE: 1064/48505 Achen et al
;   CURRENT APPLICATION NUMBER: US/09/761,636A
;   CURRENT FILING DATE: 2001-01-18
;   PRIOR APPLICATION NUMBER: US 60/176,293
;   PRIOR FILING DATE: 2000-01-18
;   PRIOR APPLICATION NUMBER: US 60/204,590
;   PRIOR FILING DATE: 2000-05-16
;   NUMBER OF SEQ ID NOS: 34
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-32
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Query Match   90.3%;   Score 65; DB 9; Length 17;
Best Local Similarity   84.6%;   Pred. No. 0.00015;
Matches   11; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFC 13
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Db   1 CASELGRSTNSFC 13

RESULT 11
US-09-761-636A-17
; Sequence 17, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-17

Query Match   84.7%;   Score 61; DB 9; Length 13;
Best Local Similarity   76.9%;   Pred. No. 0.00059;
Matches   10; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFC 13
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Db   1 CASDVGKSTNTWC 13

RESULT 12
US-09-761-636A-29
; Sequence 29, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-29

Query Match   84.7%;   Score 61; DB 9; Length 17;
Best Local Similarity   76.9%;   Pred. No. 0.00078;
Matches   10; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFC 13
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Db   1 CASDVGKSTNTWC 13

RESULT 13
US-09-761-636A-3
; Sequence 3, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid residues Val101-Thr173 of VEGF-D
US-09-761-636A-3

Query Match   75.0%;   Score 54; DB 9; Length 73;
Best Local Similarity   100.0%;   Pred. No. 0.062;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ASELGKSTNTF 12
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Db   21 ASELGKSTNTF 31

RESULT 14
US-09-761-636A-1
; Sequence 1, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid residues of Val101-Pro196 of VEGF-D
US-09-761-636A-1

Query Match   75.0%;   Score 54; DB 9; Length 96;
Best Local Similarity   100.0%;   Pred. No. 0.083;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ASELGKSTNTF 12
            |||||||||||
Db   21 ASELGKSTNTF 31

RESULT 15
US-09-956-095-3
; Sequence 3, Application US/09956095
; Patent No. US20020102260A1
; GENERAL INFORMATION:
;   APPLICANT: ACHEN, Marc G.
;   APPLICANT: STACKER, Steven A.
;   TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
;   TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
;   TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
;   TITLE OF INVENTION: VASCULARIZATION OF TISSUE
;   FILE REFERENCE: 1064/48666PC
;   CURRENT APPLICATION NUMBER: US/09/956,095
;   CURRENT FILING DATE: 2001-09-20
;   PRIOR APPLICATION NUMBER: 09/796,714
;   PRIOR FILING DATE: 2001-03-02
;   PRIOR APPLICATION NUMBER: 60/234,196
;   PRIOR FILING DATE: 2000-09-20
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-956-095-3

  Query Match   75.0%; Score 54; DB 9; Length 109;
  Best Local Similarity 100.0%; Pred. No. 0.095;
  Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ASELGKSTNTF 12
            |||||||||||
Db   29 ASELGKSTNTF 39

Search completed: September 5, 2004, 10:29:18
Job time : 37.5051 secs

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OM protein - protein search, using sw model

    Copyright   GenCore version 5.1.6
    Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: September 5, 2004, 09:55:30 ; Search time 11.5556 Seconds
                            (without alignments)
                            58.079 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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              2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
              3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
              4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
              5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
              6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	75.0	109	4	US-09-469-186-1	Sequence 1, Appli
2	54	75.0	109	4	US-09-469-185-1	Sequence 1, Appli
3	54	75.0	197	4	US-09-431-888-8	Sequence 8, Appli
4	54	75.0	325	3	US-08-915-795-3	Sequence 3, Appli
5	54	75.0	354	3	US-08-915-795-5	Sequence 5, Appli
6	51	70.8	321	3	US-08-915-795-9	Sequence 9, Appli
7	51	70.8	358	3	US-08-915-795-8	Sequence 8, Appli
8	43	59.7	83	3	US-08-875-811-2	Sequence 2, Appli
9	43	59.7	83	4	US-09-071-672-3	Sequence 3, Appli
10	43	59.7	83	4	US-09-986-119-3	Sequence 3, Appli
11	43	59.7	104	1	US-08-283-971-1	Sequence 1, Appli
12	43	59.7	104	1	US-07-921-619-1	Sequence 1, Appli
13	43	59.7	104	1	US-08-467-955-1	Sequence 1, Appli
14	43	59.7	104	1	US-08-467-955-2	Sequence 2, Appli
15	43	59.7	104	2	US-08-891-848-13	Sequence 13, Appl
16	43	59.7	104	3	US-08-875-811-1	Sequence 1, Appli
17	43	59.7	104	3	US-09-394-268-1	Sequence 1, Appli
18	43	59.7	104	3	US-09-394-268-2	Sequence 2, Appli
19	43	59.7	104	4	US-09-071-672-1	Sequence 1, Appli
20	43	59.7	104	4	US-09-687-748-1	Sequence 1, Appli
21	43	59.7	104	4	US-09-687-748-2	Sequence 2, Appli
22	43	59.7	104	4	US-08-626-288-1	Sequence 1, Appli
23	43	59.7	104	4	US-08-626-288-2	Sequence 2, Appli
24	43	59.7	104	4	US-09-095-429-1	Sequence 1, Appli
25	43	59.7	104	4	US-09-095-429-2	Sequence 2, Appli
26	43	59.7	104	4	US-09-986-119-1	Sequence 1, Appli
27	43	59.7	105	3	US-08-875-811-24	Sequence 24, Appl
28	43	59.7	105	3	US-08-875-811-26	Sequence 26, Appl
29	43	59.7	105	3	US-08-875-811-39	Sequence 39, Appl
30	43	59.7	106	3	US-08-875-811-28	Sequence 28, Appl
31	43	59.7	107	3	US-08-875-811-20	Sequence 20, Appl
32	43	59.7	107	3	US-08-875-811-30	Sequence 30, Appl
33	43	59.7	111	3	US-08-875-811-22	Sequence 22, Appl
34	43	59.7	112	3	US-08-875-811-32	Sequence 32, Appl
35	43	59.7	129	3	US-08-875-811-63	Sequence 63, Appl
36	43	59.7	251	3	US-08-875-811-59	Sequence 59, Appl
37	43	59.7	254	3	US-08-875-811-61	Sequence 61, Appl
38	43	59.7	355	3	US-08-875-811-41	Sequence 41, Appl
39	43	59.7	355	3	US-08-875-811-49	Sequence 49, Appl
40	43	59.7	355	3	US-08-875-811-57	Sequence 57, Appl
41	43	59.7	355	3	US-08-875-811-64	Sequence 64, Appl
42	43	59.7	358	3	US-08-875-811-51	Sequence 51, Appl
43	43	59.7	366	3	US-08-875-811-55	Sequence 55, Appl
44	43	59.7	379	3	US-08-875-811-43	Sequence 43, Appl
45	38	52.8	496	3	US-08-889-841B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-469-186-1
; Sequence 1, Application US/09469186
; Patent No. 6383484
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,186
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-186-1

Query Match   75.0%;   Score 54;   DB 4;   Length 109;
Best Local Similarity   100.0%;   Pred. No. 0.04%;
Matches   11;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   2 ASELGKSTNTF 12
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Db   29 ASELGKSTNTF 39

RESULT 2
US-09-469-185-1
; Sequence 1, Application US/09469185
; Patent No. 6531185
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,185
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

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;  LENGTH: 109
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-469-185-1

Query Match      75.0%;  Score 54; DB 4; Length 109;
Best Local Similarity  100.0%;  Pred. No. 0.047;
Matches  11;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       2 ASELGKSTNTF 12
           |||||||||||
Db      29 ASELGKSTNTF 39

RESULT 3
US-09-431-888-8
;  Sequence 8, Application US/09431888A
;  Patent No. 6541008
;  GENERAL INFORMATION:
;  APPLICANT: Wise, Lyn M
;  APPLICANT: Mercer, Andrew A
;  APPLICANT: Savory, Loreen J
;  APPLICANT: Fleming, Stephen B
;  APPLICANT: Stacker, Stephen
;  TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
;  TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
;  TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
;  FILE REFERENCE: Sequence Listing for 09/431,833
;  Patent No. 6541008
;  CURRENT APPLICATION NUMBER: US/09/431,888A
;  CURRENT FILING DATE: 1999-11-02
;  EARLIER APPLICATION NUMBER: 60/106,689
;  EARLIER FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: 60/106,800
;  EARLIER FILING DATE: 1998-11-03
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
;  LENGTH: 197
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-431-888-8

Query Match      75.0%;  Score 54; DB 4; Length 197;
Best Local Similarity  100.0%;  Pred. No. 0.086;
Matches  11;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       2 ASELGKSTNTF 12
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Db      45 ASELGKSTNTF 55

RESULT 4
US-08-915-795-3
;  Sequence 3, Application US/08915795
;  Patent No. 6235713
;  GENERAL INFORMATION:
;  APPLICANT: Marc G. ACHEN
;  APPLICANT: Andrew F. WILKS
;  APPLICANT: Steven A. STACKER
;  APPLICANT: Kari ALITALO
;  TITLE OF INVENTION: GROWTH FACTOR
;  NUMBER OF SEQUENCES: 11
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;  STREET: 1200 G Street, NW, Suite 700
;  CITY: Washington
;  STATE: DC
;  COUNTRY: United States of America
;  ZIP: 20005
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible

;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/915,795
;  FILING DATE:
;  CLASSIFICATION: 536
;  ATTORNEY/AGENT INFORMATION:
;  NAME: EVANS, Joseph D.
;  REGISTRATION NUMBER: 26,269
;  REFERENCE/DOCKET NUMBER: 1064/42983
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (202) 628-8800
;  TELEFAX:  (202) 628-8844
;  TELEX: N/A
INFORMATION FOR SEQ ID NO:  3:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 325 amino acids
;  TYPE: amino acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
;  HYPOTHETICAL: NO
;  ORIGINAL SOURCE:
;  TISSUE TYPE: Human Breast
US-08-915-795-3

Query Match      75.0%;  Score 54; DB 3; Length 325;
Best Local Similarity  100.0%;  Pred. No. 0.14;
Matches  11;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       2 ASELGKSTNTF 12
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Db      92 ASELGKSTNTF 102

RESULT 5
US-08-915-795-5
;  Sequence 5, Application US/08915795
;  Patent No. 6235713
;  GENERAL INFORMATION:
;  APPLICANT: Marc G. ACHEN
;  APPLICANT: Andrew F. WILKS
;  APPLICANT: Steven A. STACKER
;  APPLICANT: Kari ALITALO
;  TITLE OF INVENTION: GROWTH FACTOR
;  NUMBER OF SEQUENCES: 11
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;  STREET: 1200 G Street, NW, Suite 700
;  CITY: Washington
;  STATE: DC
;  COUNTRY: United States of America
;  ZIP: 20005
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/915,795
;  FILING DATE:
;  CLASSIFICATION: 536
;  ATTORNEY/AGENT INFORMATION:
;  NAME: EVANS, Joseph D.
;  REGISTRATION NUMBER: 26,269
;  REFERENCE/DOCKET NUMBER: 1064/42983
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (202) 628-8800
;  TELEFAX:  (202) 628-8844
;  TELEX: N/A
INFORMATION FOR SEQ ID NO:  5:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 354 amino acids
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;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ORIGINAL SOURCE:
;     TISSUE TYPE: Human Lung
US-08-915-795-5

Query Match     75.0%;  Score 54;  DB 3;  Length 354;
Best Local Similarity 100.0%;  Pred. No. 0.16;
Matches  11;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      2 ASELGKSTNTF 12
          |||||||||||
Db    121 ASELGKSTNTF 131

RESULT 6
US-08-915-795-9
; Sequence 9, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
;   APPLICANT: Marc G. ACHEN
;   APPLICANT: Andrew F. WILKS
;   APPLICANT: Steven A. STACKER
;   APPLICANT: Kari ALITALO
;   TITLE OF INVENTION: GROWTH FACTOR
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;     STREET: 1200 G Street, NW, Suite 700
;     CITY: Washington
;     STATE: DC
;     COUNTRY: United States of America
;     ZIP: 20005
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/915,795
;     FILING DATE:
;     CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;     NAME: EVANS, Joseph D.
;     REGISTRATION NUMBER: 26,269
;     REFERENCE/DOCKET NUMBER: 1064/42983
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202) 628-8800
;     TELEFAX: (202) 628-8844
;     TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 321 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   ORIGINAL SOURCE:
;     TISSUE TYPE: Mouse Lung
US-08-915-795-9

Query Match     70.8%;  Score 51;  DB 3;  Length 321;
Best Local Similarity  90.9%;  Pred. No. 0.46;
Matches  10;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;

Qy      2 ASELGKSTNTF 12
          ||||||:||||
Db    121 ASELGKTNTF 131

RESULT 7
US-08-915-795-8
; Sequence 8, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
;   APPLICANT: Marc G. ACHEN
;   APPLICANT: Andrew F. WILKS
;   APPLICANT: Steven A. STACKER
;   APPLICANT: Kari ALITALO
;   TITLE OF INVENTION: GROWTH FACTOR
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;     STREET: 1200 G Street, NW, Suite 700
;     CITY: Washington
;     STATE: DC
;     COUNTRY: United States of America
;     ZIP: 20005
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/915,795
;     FILING DATE:
;     CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;     NAME: EVANS, Joseph D.
;     REGISTRATION NUMBER: 26,269
;     REFERENCE/DOCKET NUMBER: 1064/42983
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202) 628-8800
;     TELEFAX: (202) 628-8844
;     TELEX: N/A
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 358 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   ORIGINAL SOURCE:
;     TISSUE TYPE: Mouse Lung
US-08-915-795-8

Query Match     70.8%;  Score 51;  DB 3;  Length 358;
Best Local Similarity  90.9%;  Pred. No. 0.52;
Matches  10;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;

Qy      2 ASELGKSTNTF 12
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Db    126 ASELGKTTNTF 136

RESULT 8
US-08-875-811-2
; Sequence 2, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
;   APPLICANT: Rybak, Susanna M.
;   APPLICANT: Newton, Dianne L.
;   APPLICANT: Boque, Lluis
;   APPLICANT: Wlodawer, Alexander
;   TITLE OF INVENTION: Recombinant Ribonuclease Proteins
;   NUMBER OF SEQUENCES: 64
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Center, Eighth Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
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COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/875,811
  FILING DATE: 19-FEB-1998
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: WO PCT/US97/02588
  FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 60/011,800
  FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Faris, Susan K.
  REGISTRATION NUMBER: 41,739
  REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 83 amino acids
    TYPE: amino acid
    STRANDEDNESS:
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  FEATURE:
    NAME/KEY: Peptide
    LOCATION: 1..83
    OTHER INFORMATION: /note= "Rana clone 9 peptide from Rana
                        pipiens genomic DNA"
US-08-875-811-2

Query Match   59.7%;   Score 43; DB 3; Length 83;
Best Local Similarity 61.5%; Pred. No. 2.6;
Matches   8; Conservative   1; Mismatches   1; Indels   4; Gaps   0;

Qy   1 CASELGKSTNTFC 13
          | |:|| ||||| |
Db   60 CKYKLKKSTNKFC 72

RESULT 9
US-09-071-672-3
; Sequence 3, Application US/09071672
; Patent No. 6395276
GENERAL INFORMATION:
  APPLICANT: Rybak, Susanna M.
  APPLICANT: Newton, Dianne L.
  APPLICANT: Goldenberg, David M.
  TITLE OF INVENTION: Immunotoxins Directed Against Malignant
  TITLE OF INVENTION: Cells
  NUMBER OF SEQUENCES: 3
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94111-3834
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/071,672
    FILING DATE: 01-MAY-1998
    CLASSIFICATION: 424
  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/046,895
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Weber, Ellen Lauver
  REGISTRATION NUMBER: 32,762
  REFERENCE/DOCKET NUMBER: 015280-32510US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 83 amino acids
    TYPE: amino acid
    STRANDEDNESS:
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  FEATURE:
    NAME/KEY: Protein
    LOCATION: 1..83
    OTHER INFORMATION: /note= "onc protein", positions 16-98
    OTHER INFORMATION: of SEQ ID NO:1"
US-09-071-672-3

Query Match   59.7%;   Score 43; DB 4; Length 83;
Best Local Similarity 61.5%; Pred. No. 2.6;
Matches   8; Conservative   1; Mismatches   4; Indels   4; Gaps   0;

Qy   1 CASELGKSTNTFC 13
          | |:|| ||||| |
Db   60 CKYKLKKSTNKFC 72

RESULT 10
US-09-986-119-3
; Sequence 3, Application US/09986119
; Patent No. 6653104
GENERAL INFORMATION:
  APPLICANT: Rybak, Susanna M.
  APPLICANT: Newton, Dianne L.
  APPLICANT: Goldenberg, David M.
  TITLE OF INVENTION: Immunotoxins Directed Against Malignant
                        Cells
  NUMBER OF SEQUENCES: 3
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94111-3834
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/986,119
    FILING DATE: 07-No. 6653104-2001
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/071,672
    FILING DATE: 01-MAY-1998
    APPLICATION NUMBER: US 60/046,895
    FILING DATE: 02-MAY-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Weber, Ellen Lauver
    REGISTRATION NUMBER: 32,762
    REFERENCE/DOCKET NUMBER: 015280-32510US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:

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;       LENGTH: 83 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: <Unknown>
;       TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      FEATURE:
;       NAME/KEY: Protein
;       LOCATION: 1..83
;       OTHER INFORMATION: /note= "onc protein", positions 16-98
;        of SEQ ID NO:1"
;      SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-986-119-3
;
Query Match       59.7%;  Score 43;  DB 4;  Length 83;
Best Local Similarity  61.5%;  Pred. No. 2.6;
Matches    8;  Conservative   1;  Mismatches   4;  Indels   0;  Gaps   0;

Qy    1 CASELGKSTNTFC 13
        | .:||| ||
Db   60 CKYKLKKSTNKFC 72


RESULT 11
US-08-283-971-1
; Sequence 1, Application US/08283971
; Patent No. 5529775
; GENERAL INFORMATION:
;  APPLICANT: Ardelt Ph.D, Wojciech J.
;  APPLICANT: Mikulski, Stanislaw M.
;  TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
;  NUMBER OF SEQUENCES: 1
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Mark H. Jay, P.C.
;   STREET: P.O. Box 020083, General Post Office
;   CITY: Brooklyn
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 11202-0002
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.24
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/283,971
;   FILING DATE:
;   CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/921,180
;   FILING DATE: 30-JUL-1992
;   APPLICATION NUMBER: US 07/178,118
;   FILING DATE: 06-APR-1988
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/436,141
;   FILING DATE: 13-NOV-1989
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Jay, Mark H.
;   REGISTRATION NUMBER: 27507
;   REFERENCE/DOCKET NUMBER: 5006 US
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 718-625-0399
;   TELEFAX: 718-625-0399
;   TELEX: No. 5529775 Applicable
; INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 104 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;  MOLECULE TYPE: protein
;  HYPOTHETICAL: N
;  ANTI-SENSE: N
;  FRAGMENT TYPE: N-terminal
;  ORIGINAL SOURCE:
;   ORGANISM: Rana pipiens
;   DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1
;
Query Match       59.7%;  Score 43;  DB 1;  Length 104;
Best Local Similarity  61.5%;  Pred. No. 3.3;
Matches    8;  Conservative   1;  Mismatches   4;  Indels   0;  Gaps   0;

Qy    1 CASELGKSTNTFC 13
        | .:||| ||
Db   75 CKYKLKKSTNKFC 87


RESULT 12
US-07-921-619-1
; Sequence 1, Application US/07921619
; Patent No. 5595734
; GENERAL INFORMATION:
;  APPLICANT: Ardelt Ph.D, Wojciech J.
;  APPLICANT: Mikulski, Stanislaw M.
;  TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
;  NUMBER OF SEQUENCES: 1
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Mark H. Jay, P.C.
;   STREET: P.O. Box 020083, General Post Office
;   CITY: Brooklyn
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 11202-0002
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.24
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/921,619
;   FILING DATE: 19920728
;   CLASSIFICATION: 530
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/178,118
;   FILING DATE: 06-APR-1988
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/436,141
;   FILING DATE: 13-NOV-1989
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Jay, Mark H.
;   REGISTRATION NUMBER: 27507
;   REFERENCE/DOCKET NUMBER: 5005 US
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 718-625-0399
;   TELEFAX: 718-625-0399
;   TELEX: No. 5595734 Applicable
; INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 104 amino acids
;   TYPE: AMINO ACID
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;  MOLECULE TYPE: protein
;  HYPOTHETICAL: N
;  ANTI-SENSE: N
;  FRAGMENT TYPE: N-terminal
;  ORIGINAL SOURCE:
;   ORGANISM: Rana pipiens
;   DEVELOPMENTAL STAGE: Embryo
US-07-921-619-1
;
Query Match       59.7%;  Score 43;  DB 1;  Length 104;
Best Local Similarity  61.5%;  Pred. No. 3.3;
Matches    8;  Conservative   1;  Mismatches   4;  Indels   0;  Gaps   0;

Qy    1 CASELGKSTNTFC 13
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Db   75 CKYKLKKSTNKFC 87

RESULT 13
US-08-467-955-1
; Sequence 1, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
;   APPLICANT: Ardelt Ph.D, Wojciech J.
;   TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Mark H. Jay, P.A.
;   STREET: P.O. Box E
;   CITY: Short Hills
;   STATE: New Jersey
;   COUNTRY: USA
;   ZIP: 07078-0383
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.24
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/467,955
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/178,118
;   FILING DATE: 06-APR-1988
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/436,141
;   FILING DATE: 13-NOV-1989
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/814,332
;   FILING DATE: 03-FEB-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/283,970
;   FILING DATE: 01-AUG-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Jay, Mark H.
;   REGISTRATION NUMBER: 27507
;   REFERENCE/DOCKET NUMBER: 5007 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201-912-9066
;   TELEFAX: 201-912-0442
;   TELEX: No. 5728805 Applicable
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 104 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: N
;   ANTI-SENSE: N
;   FRAGMENT TYPE: N-terminal
;   ORIGINAL SOURCE:
;   ORGANISM: Rana pipiens
;   DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-1

Query Match   59.7%; Score 43; DB 1; Length 104;
Best Local Similarity   61.5%; Pred. No. 3.3;
Matches   8; Conservative   1; Mismatches 4; Indels 0; Gaps 0;

Qy   1 CASELGKSTNTFC 13
             : | |||| ||
Db   75 CKYKLKKSTNKFC 87

RESULT 14

US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
;   APPLICANT: Ardelt Ph.D., Wojciech J.
;   TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Mark H. Jay, P.A.
;   STREET: P.O. Box E
;   CITY: Short Hills
;   STATE: New Jersey
;   COUNTRY: USA
;   ZIP: 07078-0383
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.24
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/467,955
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/178,118
;   FILING DATE: 06-APR-1988
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/436,141
;   FILING DATE: 13-NOV-1989
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/814,332
;   FILING DATE: 03-FEB-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/283,970
;   FILING DATE: 01-AUG-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Jay, Mark H.
;   REGISTRATION NUMBER: 27507
;   REFERENCE/DOCKET NUMBER: 5007 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201-912-9066
;   TELEFAX: 201-912-0442
;   TELEX: No. 5728805 Applicable
;   INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 104 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: N
;   ANTI-SENSE: N
;   FRAGMENT TYPE: N-terminal
;   ORIGINAL SOURCE:
;   ORGANISM: Rana pipiens
;   DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match   59.7%; Score 43; DB 1; Length 104;
Best Local Similarity   61.5%; Pred. No. 3.3;
Matches   8; Conservative   1; Mismatches 4; Indels 0; Gaps 0;

Qy   1 CASELGKSTNTFC 13
             : | |||| ||
Db   75 CKYKLKKSTNKFC 87

RESULT 15
US-08-891-848-13
; Sequence 13, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
;   APPLICANT: Rybak, Susanna M.

~ ; APPLICANT: Youle, Richard J.
~ ; APPLICANT: Newton, Dianne L.
~ ; APPLICANT: Nicholls, Peter J.
~ ; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
~ ; NUMBER OF SEQUENCES: 19
~ ; CORRESPONDENCE ADDRESS:
~ ; ADDRESSEE: Townsend and Townsend and Crew LLP
~ ; STREET: Two Embarcadero Center, Eighth Floor
~ ; CITY: San Francisco
~ ; STATE: California
~ ; COUNTRY: USA
~ ; ZIP: 94111-3834
~ ; COMPUTER READABLE FORM:
~ ; MEDIUM TYPE: Floppy disk
~ ; COMPUTER: IBM PC compatible
~ ; OPERATING SYSTEM: PC-DOS/MS-DOS
~ ; SOFTWARE: PatentIn Release #1.0, Version #1.30
~ ; CURRENT APPLICATION DATA:
~ ; APPLICATION NUMBER: US/08/891,848
~ ; FILING DATE: No. 5955073 yet assigned
~ ; CLASSIFICATION: 530
~ ; PRIOR APPLICATION DATA:
~ ; APPLICATION NUMBER: US 08/125,462
~ ; FILING DATE: 22-SEP-1993
~ ; PRIOR APPLICATION DATA:
~ ; APPLICATION NUMBER: US 08/014,082
~ ; FILING DATE: 04-FEB-1993
~ ; PRIOR APPLICATION DATA:
~ ; APPLICATION NUMBER: US 07/779,195
~ ; FILING DATE: 22-OCT-1991
~ ; PRIOR APPLICATION DATA:
~ ; APPLICATION NUMBER: US 07/510,696
~ ; FILING DATE: 20-APR-1990
~ ; ATTORNEY/AGENT INFORMATION:
~ ; NAME: Weber, Ellen Lauver
~ ; REGISTRATION NUMBER: 32,762
~ ; REFERENCE/DOCKET NUMBER: 015280-110310US
~ ; TELECOMMUNICATION INFORMATION:
~ ; TELEPHONE: (415) 576-0200
~ ; TELEFAX: (415) 576-0300
~ ; INFORMATION FOR SEQ ID NO: 13:
~ ; SEQUENCE CHARACTERISTICS:
~ ; LENGTH: 104 amino acids
~ ; TYPE: amino acid
~ ; STRANDEDNESS:
~ ; TOPOLOGY: linear
~ ; MOLECULE TYPE: protein
~ ; FEATURE:
~ ; NAME/KEY: Protein
~ ; LOCATION: 1..104
~ ; OTHER INFORMATION: /label= Onc
~ ; OTHER INFORMATION: /note= "Onconase from Rana pipiens"
US-08-891-848-13

Query Match   59.7%; Score 43; DB 2; Length 104;
Best Local Similarity 61.5%; Pred. No. 3.3;
Matches   8; Conservative   1; Mismatches   4; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFC 13
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Db   75 CKYKLKKSTNKFC 87

Search completed: September 5, 2004, 10:21:56
Job time : 12.5556 secs

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                GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:  September 5, 2004, 09:47:29 ; Search time 6.14141 Seconds
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Title:          US-09-761-636A-6
Perfect score:  46
Sequence:       1 CNEESLIC 8

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:      283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      PIR_78:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	78.3	120	2	A33787	vascular endotheli
2	36	78.3	133	2	B49530	vascular endotheli
3	36	78.3	146	2	S57956	ovine vascular end
4	36	78.3	190	2	B40080	vascular endotheli
5	36	78.3	1115	2	A45761	Ca2+-transporting
6	35		4427	2	PN0637	polyketide synthas
7	34.5	75.0	351	2	T42421	hypothetical prote
8	34.5	75.0	1778	2	T50074	probable nucleopor
9	34	73.9	295	2	H71078	probable cation ef
10	34	73.9	501	1	A40938	cytochrome P450 ib
11	34	73.9	642	2	T51421	L-aspartate oxidas
12	34	73.9	1722	1	I78879	retinoblastoma bin
13	33	71.7	190	2	B44881	vascular endotheli
14	33	71.7	190	2	A35987	glioma-derived vas
15	33	71.7	214	2	A44881	vascular endotheli
16	33	71.7	291	2	AF0123	probable antigenic
17	33	71.7	325	2	G90130	transcription init
18	33	71.7	350	2	D69143	LPS biosynthesis R
19	33	71.7	551	2	JC7562	glioblastoma RING
20	33	71.7	1786	1	MMHUB1	laminin beta-1 cha
21	32	69.6	169	2	S76289	hypothetical prote
22	32	69.6	183	2	E72459	hypothetical prote
23	32	69.6	190	2	S52130	vascular endotheli
24	32	69.6	232	2	A41551	vascular endotheli
25	32	69.6	272	2	S13587	malate dehydrogena
26	32	69.6	290	2	G97328	uncharacterized co
27	32	69.6	338	2	E86465	hypothetical prote
28	32	69.6	358	2	A82206	protein-glutamate
29	32	69.6	376	2	B72321	conserved hypothet
30	32	69.6	399	2	H87486	1-deoxy-D-xylulose
31	32	69.6	429	2	JH0151	malate dehydrogena
32	32	69.6	429	2	S13588	malate dehydrogena
33	32	69.6	429	2	T16656	hypothetical prote
34	32	69.6	430	2	S17781	malate dehydrogena
35	32	69.6	432	1	DEMZMC	malate dehydrogena
36	32	69.6	432	2	S20743	malate dehydrogena
37	32	69.6	435	2	S52268	malate dehydrogena
38	32	69.6	441	2	S33066	malate dehydrogena
39	32	69.6	441	2	S38346	malate dehydrogena
40	32	69.6	463	2	T15416	hypothetical prote
41	32	69.6	765	2	AF0118	probable kinase YP
42	32	69.6	766	2	AG0179	hypothetical prote
43	32	69.6	1044	2	H97186	glycosyltransferas
44	32	69.6	1047	2	T21306	hypothetical prote
45	32	69.6	1124	2	H88772	protein F23B2.4 [i

ALIGNMENTS

RESULT 1
A33787
vascular endothelial growth factor (version 1) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 05-Nov-1999
C;Accession: A33787
R;Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisp
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
A;Title: Vascular endothelial growth factor: a new member of the platelet-derived growth
A;Reference number: A33787; MUID:90121225; PMID:2610687
A;Accession: A33787
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <TIS>
A;Cross-references: GB:M33750; NID:g163810; PIDN:AAA30805.1; PID:g163811
C;Keywords: alternative splicing

Query Match   78.3%; Score 36; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy    1 CNEESLIC 8
          ||:||||
Db   60 CNDESLEC 67
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RESULT 2
B49530
vascular endothelial growth factor homolog A2R, 14.7K - Orf virus
C;Species: Orf virus
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: B49530
R;Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
J. Virol. 68, 84-92, 1994
A;Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus orf
A;Reference number: A49530; MUID:94076465; PMID:8254780
A;Contents: NZ2
A;Accession: B49530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <LYT>
A;Cross-references: GB:S67520; NID:g456897; PIDN:AAB29220.1; PID:g456899
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:141420, NCBIP:141425)

Query Match   78.3%; Score 36; DB 2; Length 133;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy    1 CNEESLIC 8
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Db   71 CNDESLEC 78
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RESULT 3
S57956
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C;Accession: S57956
R;Redmer, D.A.; Dai, Y.; Li, J.; Jones, S.C.; Moor, R.M.
submitted to the EMBL Data Library, July 1995
A;Reference number: S57956
A;Accession: S57956
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <RED>
A;Cross-references: EMBL:X89506; NID:g899350; PIDN:CAA61677.1; PID:g899351

Query Match   78.3%;   Score 36; DB 2; Length 146;
Best Local Similarity 75.0%;   Pred. No. 13;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
        ||:|||
Db   86 CNDESLEC 93

RESULT 4
B40080
vascular endothelial growth factor precursor (version 2) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Nov-1999
C;Accession: B40080; B33787; A33255
R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1306-1309, 1989
A;Reference number: A40080; MUID:90069608; PMID:2479986
A;Accession: B40080
A;Molecule type: mRNA
A;Residues: 1-190 <LEU>
A;Cross-references: GB:M32976; NID:g163006; PIDN:AAA30502.1; PID:g163007
R;Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisp
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
A;Title: Vascular endothelial growth factor: a new member of the platelet-derived growth
A;Reference number: A33787; MUID:90121225; PMID:2610687
A;Accession: B33787
A;Molecule type: mRNA
A;Residues: 27-190 <TIS>
A;Cross-references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809
R;Ferrara, N.; Henzel, W.J.
Biochem. Biophys. Res. Commun. 161, 851-858, 1989
A;Title: Pituitary follicular cells secrete a novel heparin-binding growth factor specif
A;Reference number: A33255; MUID:89286596; PMID:2735925
A;Accession: A33255
A;Molecule type: protein
A;Residues: 27-31 <FER>
C;Keywords: alternative splicing; glycoprotein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-190/Product: vascular endothelial growth factor #status predicted <MAT>
F;100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   78.3%;   Score 36; DB 2; Length 190;
Best Local Similarity 75.0%;   Pred. No. 16;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
        ||:|||
Db   86 CNDESLEC 93

RESULT 5
A45761
Ca2+-transporting ATPase (EC 3.6.3.8) - Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 19-Apr-2002
C;Accession: A45761
R;Murakami, K.; Tanabe, K.; Takada, S.
J. Cell Sci. 97, 487-495, 1990
A;Title: Structure of a Plasmodium yoelii gene-encoded protein homologous to the Ca(2+)-
A;Reference number: A45761; MUID:91161669; PMID:2150071
A;Accession: A45761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1115 <MUR>
A;Cross-references: GB:X55197; NID:g10097; PIDN:CAA38982.1; PID:g10098
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: hydrolase
F;689-866/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match   78.3%;   Score 36; DB 2; Length 1115;
Best Local Similarity 62.5%;   Pred. No. 75;
Matches   5; Conservative   5; Mismatches   2; Indels   1; Gaps   0;

Qy   1 CNEESLIC 8
        ||:| :|
Db 486 CNEASILC 493

RESULT 6
PN0637
polyketide synthase pksL - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 19-May-1994 #sequence_revision 06-Feb-1995 #text_change 03-Nov-2000
C;Accession: S25021; PN0637; B69679
R;Scotti, C.; Piatti, M.; Cuzzoni, A.; Tognoni, A.; Grandi, G.; Galizzi, A.
submitted to the EMBL Data Library, July 1992
A;Description: A Bacillus subtilis large ORF coding for a polypeptide highly similar to
A;Reference number: S25021
A;Accession: S25021
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4427 <SCO>
A;Cross-references: EMBL:Z14098; NID:g40057; PIDN:CAA78479.1; PID:g40058
R;Scotti, C.; Piatti, M.; Cuzzoni, A.; Perani, P.; Tognoni, A.; Grandi, G.; Galizzi, A.
Gene 130, 65-71, 1993
A;Title: A Bacillus subtilis large ORF coding for a polypeptide highly similar to polyke
A;Reference number: PN0637; MUID:93345824; PMID:8344529
A;Accession: PN0637
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 184-282;382-850;926-1115;1409-1648;1665-1761;1876-2344;2469-2560;2609-2702;...
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y., M.; Ogawa, A.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, H.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B69679
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-4427 <KUN>
A;Cross-references: GB:Z99113; GB:AL009126; NID:g2634090; PIDN:CAB13602.1; PID:g2634102
A;Experimental source: strain 168
C;Comment: This enzyme is composed of four synthase units. Unit1 comprises beta-ketosyn
acyl-carrier protein domains. Unit3 comprises beta-ketosynthase, acyl-carrier protein a
C;Genetics:
A;Genetics:
A;Gene: pksL; pksx

```
C;Superfamily: Bacillus subtilis polyketide synthase pksL; 3-oxoacyl-[acyl-carrier-prote
C;Keywords: acyltransferase; carrier protein
F;343-758/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
F;1410-1591/Domain: short-chain alcohol dehydrogenase homology <SAD1>
F;1836-2252/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>
F;2485-2559/Domain: acyl carrier protein homology <ACP1>
F;2626-2700/Domain: acyl carrier protein homology <ACP2>
F;2783-3181/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS3>
F;3576-3774/Domain: short-chain alcohol dehydrogenase homology <SAD2>
F;3852-3922/Domain: acyl carrier protein homology <ACP3>
F;3992-4372/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS4>

    Query Match      76.1%;   Score 35;   DB 2;   Length 4427;
    Best Local Similarity   62.5%;   Pred. No. 3.7e+02;
    Matches    5;   Conservative    1;   Mismatches    2;   Indels    0;   Gaps    0;

Qy    1 CNEESLIC 8
        ||||| :|
Db 1205 CNEEGQVC 1212

RESULT 7
T42421
hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T42421
R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T42421
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-351 <YOS>
A;Cross-references: EMBL;D89145; NID:g1749497; PIDN:BAA13807.1; PID:g1749498
A;Experimental source: strain PR745

    Query Match      75.0%;   Score 34.5;   DB 2;   Length 351;
    Best Local Similarity   72.7%;   Pred. No. 53;
    Matches    8;   Conservative    0;   Mismatches    0;   Indels    3;   Gaps    1;

Qy    1 CNEESL---IC 8
        |||||  ||
Db  321 CNEESLTDAIC 331

RESULT 8
T50074
probable nucleoporin [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C;Accession: T50074
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
submitted to the EMBL Data Library, December 1999
A;Reference number: Z25034
A;Accession: T50074
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1778 <MCD>
A;Cross-references: EMBL;AL133357; PIDN:CAB62415.1; GSPDB:GN00066; SPDB:SPAC1486.05
A;Experimental source: strain 972h(-); cosmid c1486
C;Genetics:
A;Gene: SPDB:SPAC1486.05
A;Map position: 1
A;Introns: 139/2

    Query Match      75.0%;   Score 34.5;   DB 2;   Length 1778;
    Best Local Similarity   72.7%;   Pred. No. 2.1e+02;
    Matches    8;   Conservative    0;   Mismatches    0;   Indels    3;   Gaps    1;

Qy    1 CNEESL---IC 8
        |||||  ||
Db 1748 CNEESLTDAIC 1758

RESULT 9
H71078
probable cation efflux system protein czcD - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: H71078
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
  M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: H71078
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-295 <KAW>
A;Cross-references: GB;AP000004; NID:g3236131; PIDN:BAA29990.1; PID:g3257307
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0896
C;Superfamily: zinc transporter ZnT-2

    Query Match      73.9%;   Score 34;   DB 2;   Length 295;
    Best Local Similarity   62.5%;   Pred. No. 57;
    Matches    5;   Conservative    2;   Mismatches    2;   Indels    1;   Gaps    0;

Qy    1 CNEESLIC 8
        |:|:|:||
Db  283 CKEKSMIC 290

RESULT 10
A40938
cytochrome P450 ib - rabbit
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A40938
R;Kikuta, Y.; Sogawa, K.; Haniu, M.; Kinosaki, M.; Kusunose, E.; Nojima, Y.; Yamamoto, S
J. Biol. Chem. 266, 17821-17825, 1991
A;Title: A novel species of cytochrome P-450 (P-450-ib) specific for the small intestine
A;Reference number: A40938; MUID:92011499; PMID:1717443
A;Accession: A40938
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-501 <KIK>
A;Cross-references: GB;D90405; NID:g217717; PIDN:BAA14401.1; PID:g217718
C;Genetics:
A;Gene: CYP2J1
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;308-469/Domain: cytochrome P450 homology <CYP>
F;447/Binding site: heme iron (Cys) (axial ligand) #status predicted

    Query Match      73.9%;   Score 34;   DB 1;   Length 501;
    Best Local Similarity   85.7%;   Pred. No. 89;
    Matches    6;   Conservative    1;   Mismatches    0;   Indels    0;   Gaps    0;

Qy    2 NEESLIC 8
        |||:|||
Db  297 NEENLIC 303

RESULT 11
T51421
L-aspartate oxidase-like protein - Arabidopsis thaliana
N;Alternate names: protein T9L3 60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: T51421
```

R.Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; New
submitted to the Protein Sequence Database, August 2000
A;Reference number: Z5394
A;Accession: T51421
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-642 <SAT>
A;Cross-references: EMBL:AL391149
A;Experimental source: cultivar Columbia; BAC clone T9L3
C;Genetics:
A;Map position: 5
A;Introns: 43/2; 158/3; 239/3; 258/3; 278/3; 299/2
A;Note: T9L3_60
C;Superfamily: fumarate reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homology; f

Query Match   73.9%; Score 34; DB 2; Length 642;
Best Local Similarity   50.0%; Pred. No. 1.1e+02;
Matches   4; Conservative   4; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
            |:||:::|
Db   154 CDEETVVC 161

RESULT 12
I78879
retinoblastoma binding protein 2 - human
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: I78879; S16954
R.Fattaey, A.R.; Helin, K.; Dembski, M.S.; Dyson, N.; Harlow, E.; Vuocolo, G.A.; Hanobik
Oncogene 8, 3149-3156, 1993
A;Title: Characterization of the retinoblastoma binding proteins RBP1 and RBP2.
A;Reference number: I58383; MUID:94020841; PMID:8414517
A;Accession: I78879
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1722 <PAT>
A;Cross-references: GB:S66431; NID:g435777; PIDN:AAB28544.1; PID:g435778
R.Defeo-Jones, D.; Huang, P.S.; Jones, R.E.; Haskell, K.M.; Vuocolo, G.A.; Hanobik, M.G.
Nature 352, 251-254, 1991
A;Title: Cloning of cDNAs for cellular proteins that bind to the retinoblastoma gene pro
A;Reference number: S16953; MUID:91312450; PMID:1857421
A;Accession: S16954
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1102-1562,'KKK' <DEF>
C;Genetics:
A;Gene: GDB:RBP2
A;Cross-references: GDB:119548; OMIM:180280
A;Map position: 3q21-3qter
C;Superfamily: human retinoblastoma binding protein 2

Query Match   73.9%; Score 34; DB 1; Length 1722;
Best Local Similarity   62.5%; Pred. No. 2.6e+02;
Matches   5; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
            |||||:|
Db   692 CNPERLVC 699

RESULT 13
B44881
vascular endothelial growth factor-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Nov-1999
C;Accession: B44881; A43351; A61029
R.Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A;Title: Expression of vascular endothelial growth factor during embryonic angiogenesis
A;Reference number: A44881; MUID:92274860; PMID:1592003
A;Accession: B44881

A;Molecule type: mRNA
A;Residues: 1-190 <BRE>
A;Cross-references: GB:S38083; NID:g249858; PIDN:AAB22253.1; PID:g249859
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBIP:107623)
R.Claffey, K.P.; Wilkison, W.O.; Spiegelman, B.M.
J. Biol. Chem. 267, 16317-16322, 1992
A;Title: Vascular endothelial growth factor. Regulation by cell differentiation and acti
A;Reference number: A43351; MUID:92355593; PMID:1644816
A;Accession: A43351
A;Molecule type: mRNA
A;Residues: 1-116, 'ER',119-190 <CLA>
A;Cross-references: GB:M95200; NID:g202350; PIDN:AAA40547.1; PID:g202351
A;Note: sequence extracted from NCBI backbone (NCBIN:110665, NCBIP:110675)
R.Rosenthal, R.A.; Megyesi, J.F.; Henzel, W.J.; Ferrara, N.; Folkman, J.
Growth Factors 4, 53-59, 1990
A;Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelial g
A;Reference number: A61029; MUID:9197543; PMID:2085441
A;Accession: A61029
A;Molecule type: protein
A;Residues: 27-38 <ROS>
C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein; mit

Query Match   71.7%; Score 33; DB 2; Length 190;
Best Local Similarity   62.5%; Pred. No. 60;
Matches   5; Conservative   2; Mismatches   2; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
            |||:||:|
Db   86 CNDEALEC 93

RESULT 14
A35987
glioma-derived vascular endothelial cell growth factor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Nov-1999
C;Accession: A35987
R.Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Hope
Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990
A;Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is h
A;Reference number: A35987; MUID:9207249; PMID:2320579
A;Accession: A35987
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <CON>
A;Cross-references: GB:M32167; NID:g204287; PIDN:AAA41211.1; PID:g204288

Query Match   71.7%; Score 33; DB 2; Length 190;
Best Local Similarity   62.5%; Pred. No. 60;
Matches   5; Conservative   2; Mismatches   2; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
            |||:||:|
Db   86 CNDEALEC 93

RESULT 15
A44881
vascular endothelial growth factor-3 precursor - mouse
N;Contains: vascular endothelial growth factor-2; vascular permeability factor
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C;Accession: A44881; C44881; A60932; S52136
R.Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A;Title: Expression of vascular endothelial growth factor during embryonic angiogenesis
A;Reference number: A44881; MUID:92274860; PMID:1592003
A;Accession: A44881
A;Molecule type: mRNA
A;Residues: 1-214 <BRE>
A;Cross-references: GB:S37052; NID:g249856; PIDN:AAB22252.1; PID:g249857
A;Experimental source: embryo

A;Note: sequence extracted from NCBI backbone (NCBIN:104677, NCBIP:104678)
A;Accession: C44881
A;Molecule type: mRNA
A;Residues: 1-140,209-214 <BR2>
A;Cross-references: GB:S38100; NID:g249860; PIDN:AAB22254.1; PID:g249861
A;Note: sequence extracted from NCBI backbone (NCBIN:107624, NCBIP:107625)
R;Clauss, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; Pan, Y.C.
J. Exp. Med. 172, 1535-1545, 1990
A;Title: Vascular permeability factor: a tumor-derived polypeptide that induces endothel
A;Reference number: A60932; MUID:91079755; PMID:2258694
A;Accession: A60932
A;Molecule type: protein
A;Residues: 27-33 <CLA>
R;Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
Biochim. Biophys. Acta 1224, 365-370, 1994
A;Title: Enhanced expression of multiple forms of VEGF is associated with spontaneous im
A;Reference number: S52136; MUID:95101726; PMID:7803491
A;Accession: S52136
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-46 <SUG>
C;Comment: Homodimers could be demonstrated for recombinant VEGF-2 but not VEGF-3.
C;Keywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homodimer;
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-214/Product: vascular endothelial growth factor-3 #status experimental <MAT>

Query Match   71.7%;   Score 33; DB 2; Length 214;
Best Local Similarity   62.5%;   Pred. No. 66;
Matches   5; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
          || :|:||
Db   86 CNDEALEC 93

Search completed: September 5, 2004, 10:01:16
Job time : 8.14141 secs

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                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:    September 5, 2004, 09:38:39 ; Search time 3.63636 Seconds
                                        (without alignments)
                                        114.554 Million cell updates/sec

Title:        US-09-761-636a-6
Perfect score: 46
Sequence:     1 CNEESLIC 8

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:     141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:       141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                            SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	100.0	354	1	VEGD_HUMAN	O43915 homo sapien
2	40	87.0	326	1	VEGD_RAT	O35251 rattus norv
3	36	78.3	133	1	VEGH_ORFN2	P52584 orf virus (
4	36	78.3	146	1	VEGA_SHEEP	P50412 ovis aries
5	36	78.3	164	1	VEGA_CAVPO	P26617 cavia porce
6	36	78.3	190	1	VEGA_BOVIN	P15691 bos taurus
7	36	78.3	358	1	VEGD_MOUSE	P97946 mus musculu
8	35	76.1	495	1	FASC_STRPU	Q05634 strongyloce
9	35	76.1	4427	1	PKSL_BACSU	Q05470 bacillus su
10	34.5	75.0	1778	1	N189_SCHPO	Q9utk4 schizosacch
11	34	73.9	500	1	CPJ1_RABIT	P52786 oryctolagus
12	34	73.9	501	1	CPJ6_MOUSE	O54750 mus musculu
13	34	73.9	502	1	CPJ3_RAT	P51590 rattus norv
14	34	73.9	545	1	LGI2_HUMAN	Q8n0v4 homo sapien
15	34	73.9	550	1	LGI2_MOUSE	Q8k4z0 mus musculu
16	34	73.9	1722	1	RBB2_HUMAN	P29375 homo sapien
17	33	71.7	214	1	VEGA_MOUSE	Q00731 mus musculu
18	33	71.7	214	1	VEGA_RAT	P16612 rattus norv
19	33	71.7	404	1	ARGJ_HELHP	Q93ej3 h arginine
20	33	71.7	508	1	CPT7_HORSE	Q95328 equus cabal
21	33	71.7	551	1	RN27_HUMAN	Q9bzr9 homo sapien
22	33	71.7	551	1	RN27_MOUSE	Q99pj2 mus musculu
23	33	71.7	1786	1	LMB1_HUMAN	P07942 homo sapien
24	32	69.6	138	1	PA26_TRIGA	P70088 trimeresuru
25	32	69.6	190	1	VEGA_HORSE	Q9gkr0 equus cabal
26	32	69.6	190	1	VEGA_PIG	P49151 sus scrofa
27	32	69.6	214	1	VEGA_CANFA	Q9myv3 canis famil
28	32	69.6	232	1	VEGA_HUMAN	P15692 homo sapien
29	32	69.6	376	1	DXR_THEMA	Q9wzz1 thermotoga
30	32	69.6	399	1	DXR_CAUCR	Q9a709 caulobacter
31	32	69.6	429	1	MDHP_SORBI	P17606 sorghum bic
32	32	69.6	432	1	MDHP_MAIZE	P15719 zea mays (m
33	32	69.6	432	1	MDHQ_SORBI	P37229 sorghum bic
34	32	69.6	435	1	MDHP_SPIOL	P52426 spinacia ol
35	32	69.6	437	1	MDHP_MEDSA	O48902 medicago sa
36	32	69.6	441	1	MDHP_MESCR	Q05145 mesembryant
37	32	69.6	441	1	MDHP_PEA	P21528 pisum sativ
38	32	69.6	453	1	MDHP_FLABI	P46489 flaveria bi
39	31	67.4	51	1	YDAF_ECOLI	P38395 escherichia
40	31	67.4	82	1	VG13_HSV11	Q00166 ictalurid h
41	31	67.4	171	1	NIDM_HUMAN	O96000 homo sapien
42	31	67.4	218	1	PURQ_METTH	O26270 methanobact
43	31	67.4	231	1	TRMD_MYCGE	P47683 mycoplasma
44	31	67.4	251	1	Y206_CHLPN	Q9z8x8 chlamydia p
45	31	67.4	291	1	ISPE_CHLCV	Q821x0 chlamydophi

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                            ALIGNMENTS

RESULT 1
VEGD_HUMAN
ID   VEGD_HUMAN              STANDARD;      PRT;    354 AA.
AC   O43915;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF).
GN   FIGF OR VEGFD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=97349118; PubMed=9205122;
RA   Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=98140120; PubMed=9479493;
RA   Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA   Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT   "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT   between the PIGA and the GRPR genes.";
RL   Genomics 47:207-216(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98118549; PubMed=9435229;
RA   Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,
RA   Alitalo K., Stacker S.A.;
RT   "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT   tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smailus D.E.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
RX   MEDLINE=20011413; PubMed=10542248;
RA   Stacker S.A., Stenvers K.L., Caesar C., Vitali A., Domagala T.,
RA   Nice E.C., Roufail S., Simpson R.J., Moritz R., Karpanen T.,
RA   Alitalo K., Achen M.G.;
RT   "Biosynthesis of vascular endothelial growth factor-D involves
RT   proteolytic processing which generates non-covalent homodimers.";
RL   J. Biol. Chem. 274:32127-32136(1999).
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC       and endothelial cell growth, stimulating their proliferation and
CC       migration and also has effects on the permeability of blood
CC       vessels. May function in the formation of the venous and lymphatic
CC       vascular systems during embryogenesis, and also in the maintenance
CC       of differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in lung, heart, small
CC       intestine and fetal lung, and at lower levels in skeletal muscle,
CC       colon, and pancreas.
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC       linked by disulfide bonds before secretion. The fully processed
CC       VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC       bound by non-covalent interactions.
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
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DR   EMBL; D89630; BAA24264.1; -.
DR   EMBL; Y12863; CAA73370.1; -.
DR   EMBL; Y12864; CAA73371.1; -.
DR   EMBL; Y12865; CAA73371.1; JOINED.
DR   EMBL; Y12866; CAA73371.1; JOINED.
DR   EMBL; Y12867; CAA73371.1; JOINED.
DR   EMBL; Y12868; CAA73371.1; JOINED.
DR   EMBL; Y12869; CAA73371.1; JOINED.
DR   EMBL; Y12870; CAA73371.1; JOINED.
DR   EMBL; AJ000185; CAA03942.1; -.
DR   EMBL; BC027948; AAH27948.1; -.
DR   HSSP; P15692; 1VPP.
DR   Genew; HGNC:3708; FIGF.
DR   MIM; 300091; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005161; F:platelet-derived growth factor receptor bin. . .; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR0000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 3.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF_1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL        1     21       POTENTIAL.
FT   PROPEP       22     88       OR 99 (IN A MINOR FORM).
FT   CHAIN        89    205       VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP      206    354
FT   DOMAIN      222    318       4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT                                X(1,3)-C.
FT   REPEAT      222    237       1 (APPROXIMATE).
FT   REPEAT      258    273       2.
FT   REPEAT      277    293       3.
FT   REPEAT      301    318       4.
FT   DISULFID    111    153       BY SIMILARITY.
FT   DISULFID    142    189       BY SIMILARITY.
FT   DISULFID    146    191       BY SIMILARITY.
FT   DISULFID    136    136       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    145    145       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    155    155       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    185    185       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    287    287       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE    354 AA;  40444 MW;  204BD769D735173B CRC64;

Query Match             100.0%;  Score 46;  DB 1;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 0.083;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CNEESLIC 8
              ||||||||
Db        146 CNEESLIC 153


RESULT 2
VEGD_RAT
ID   VEGD_RAT       STANDARD;      PRT;   326 AA.
AC   O35251;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF).
GN   FIGF OR VEGFD.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Yamada Y., Hirata Y., Nezu J., Shimane M.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC       and endothelial cell growth, stimulating their proliferation and
CC       migration and also has effects on the permeability of blood
CC       vessels. May function in the formation of the venous and lymphatic
CC       vascular systems during embryogenesis, and also in the maintenance
CC       of differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-3 (Flt4) receptor (By similarity).
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC       linked by disulfide bonds before secretion. The fully processed
CC       VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC       bound by non-covalent interactions (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
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DR   EMBL; AF014827; AAB66557.1; -.
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DR   HSSP; P15692; 1VPP.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 1.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL       1     21       POTENTIAL.
FT   PROPEP      22     93       POTENTIAL.
FT   CHAIN       94    210       VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP     211    326       POTENTIAL.
FT   DOMAIN     227    317       4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT                               X(1,3)-C.
FT   REPEAT     227    242       1 (APPROXIMATE).
FT   REPEAT     263    278       2.
FT   REPEAT     282    298       3.
FT   REPEAT     306    317       4 (INCOMPLETE).
FT   DISULFID   116    158       BY SIMILARITY.
FT   DISULFID   147    194       BY SIMILARITY.
FT   DISULFID   151    196       BY SIMILARITY.
FT   DISULFID   141    141       INTERCHAIN (BY SIMILARITY).
FT   DISULFID   150    150       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   160    160       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   190    190       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   292    292       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   326 AA;  37112 MW;  1261AFA373596C00 CRC64;

Query Match             87.0%;
Best Local Similarity   75.0%;     Score 40;  DB 1;  Length 326;
Matches    6;  Conservative   2;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      1 CNEESLIC 8
            ||||::|
Db    151 CNEESVMC 158


RESULT 3
VEGH_ORFN2
ID   VEGH_ORFN2     STANDARD;     PRT;   133 AA.
AC   P52584;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor homolog precursor.
GN   A2R.
OS   Orf virus (strain NZ2) (OV NZ-2).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=10259;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94076465; PubMed=8254780;
RA   Lyttle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.;
RT   "Homologs of vascular endothelial growth factor are encoded by the
RT   poxvirus orf virus.";
RL   J. Virol. 68:84-92(1994).
CC   -!- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   -------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------
DR   EMBL; S67520; AAB29220.2; -.
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DR   HSSP; P15692; 1VPP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL       1     20       POTENTIAL.
FT   CHAIN       21    133       VASCULAR ENDOTHELIAL GROWTH FACTOR
FT                               HOMOLOG.
FT   DISULFID    36     78       BY SIMILARITY.
FT   DISULFID    67    112       BY SIMILARITY.
FT   DISULFID    71    114       BY SIMILARITY.
FT   DISULFID    61     61       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    70     70       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    85     85       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   133 AA;  14715 MW;  917C0F6883030C39 CRC64;

Query Match             78.3%;
Best Local Similarity   75.0%;     Pred. No. 2.9;     Score 36;  DB 1;  Length 133;
Matches    6;  Conservative   1;  Mismatches   1;  Indels   1;  Gaps   0;

Qy      1 CNEESLIC 8
            ||:|||:|
Db     71 CNDESLEC 78


RESULT 4
VEGA_SHEEP
ID   VEGA_SHEEP     STANDARD;     PRT;   146 AA.
AC   P50412;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE   permeability factor) (VPF).
GN   VEGF OR VEGFA.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=kidney;
RX   MEDLINE=97117958; PubMed=8958842;
RA   Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,
RA   Reynolds L.P., Moor R.M.;
RT   "Characterization and expression of vascular endothelial growth
RT   factor (VEGF) in the ovine corpus luteum.";
RL   J. Reprod. Fertil. 108:157-165(1996).
CC   -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC       endothelial cell growth. It induces endothelial cell
CC       proliferation, promotes cell migration, inhibits apoptosis, and
CC       induces permeabilization of blood vessels. It binds to the
CC       VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC       heparin (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC       with PlGF (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   -------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------
DR   EMBL; X89506; CAA61677.1; -.
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DR   PIR; S57956, S57956.
DR   HSSP; P15692; 1VPF.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW   Heparin-binding; Multigene family.
FT   SIGNAL   1   26   BY SIMILARITY.
FT   CHAIN   27   146   VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT   DISULFID   51   93   BY SIMILARITY.
FT   DISULFID   82   127   BY SIMILARITY.
FT   DISULFID   86   129   BY SIMILARITY.
FT   DISULFID   76   76   INTERCHAIN (BY SIMILARITY).
FT   DISULFID   85   85   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   100   100   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   146 AA;   17247 MW; 4E792CB557F91760 CRC64;

Query Match   78.3%;   Score 36; DB 1; Length 146;
Best Local Similarity   75.0%;   Pred. No. 3.1;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
          ||:|||
Db   86 CNDESLEC 93

RESULT 5
VEGA_CAVPO
ID   VEGA_CAVPO   STANDARD;   PRT;   164 AA.
AC   P26617;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor A (VEGF-A) (Vascular permeability
DE   factor) (VPF).
GN   VEGF OR VEGFA.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bile duct;
RA   Berse B.;
RL   Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Growth factor active in angiogenesis, and endothelial
CC   cell growth. Induces endothelial proliferation and vascular
CC   permeability (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC   with PlGF (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC   to the extracellular matrix unless released by heparin (By
CC   similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; M84230; AAA37057.1; -.
DR   HSSP; P15692; 1VGH.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.

DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Angiogenesis; Growth factor; Glycoprotein.
FT   DISULFID   25   67   BY SIMILARITY.
FT   DISULFID   56   101   BY SIMILARITY.
FT   DISULFID   60   103   BY SIMILARITY.
FT   DISULFID   50   50   INTERCHAIN (BY SIMILARITY).
FT   DISULFID   59   59   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   74   74   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   164 AA;   19330 MW; 9EB86A81A9D5DCA4 CRC64;

Query Match   78.3%;   Score 36; DB 1; Length 164;
Best Local Similarity   75.0%;   Pred. No. 3.6;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
          ||:|||
Db   60 CNDESLEC 67

RESULT 6
VEGA_BOVIN
ID   VEGA_BOVIN   STANDARD;   PRT;   190 AA.
AC   P15691;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE   permeability factor) (VPF).
GN   VEGF OR VEGFA.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
RX   MEDLINE=90069608; PubMed=2479986;
RA   Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
RT   "Vascular endothelial growth factor is a secreted angiogenic
RT   mitogen.";
RL   Science 246:1306-1309(1989).
RN   [2]
RP   SEQUENCE OF 27-190 FROM N.A. (ISOFORMS ALPHA AND BETA).
RX   MEDLINE=90121225; PubMed=2610687;
RA   Tischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J.,
RA   Lau K., Crisp T., Fiddes J.C., Abraham J.A.;
RT   "Vascular endothelial growth factor: a new member of the platelet-
RT   derived growth factor gene family.";
RL   Biochem. Biophys. Res. Commun. 165:1198-1206(1989).
RN   [3]
RP   SEQUENCE OF 27-31.
RX   MEDLINE=89286596; PubMed=2735925;
RA   Ferrara N., Henzel W.J.;
RT   "Pituitary follicular cells secrete a novel heparin-binding growth
RT   factor specific for vascular endothelial cells.";
RL   Biochem. Biophys. Res. Commun. 161:851-858(1989).
CC   -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC   endothelial cell growth. It induces endothelial cell
CC   proliferation, promotes cell migration, inhibits apoptosis, and
CC   induces permeabilization of blood vessels. It binds to the
CC   VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC   heparin (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC   with PlGF (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC   to the extracellular matrix unless released by heparin (By
CC   similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=2;

CC   Name=Alpha;
CC   IsoId=P15691-1; Sequence=Displayed;
CC   Name=Beta;
CC   IsoId=P15691-2; Sequence=VSP_004613, VSP_004614;
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   ---
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CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; M32976; AAA30502.1; -.
DR   EMBL; M31836; AAA30804.1; -.
DR   EMBL; M33750; AAA30805.1; -.
DR   PIR; A33787; A33787.
DR   PIR; B40080; B40080.
DR   HSSP; P15692; 1VGH.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW   Heparin-binding; Alternative splicing; Multigene family.
FT   SIGNAL   1   26
FT   CHAIN   27   190   VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT   DISULFID   51   93   BY SIMILARITY.
FT   DISULFID   82   127   BY SIMILARITY.
FT   DISULFID   86   129   BY SIMILARITY.
FT   DISULFID   76   76   INTERCHAIN (BY SIMILARITY).
FT   DISULFID   85   85   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   100   100   N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC   139   183   Missing (in isoform Beta).
FT   /FTId=VSP_004613.
FT   VARSPLIC   184   184   R -> K (in isoform Beta).
FT   /FTId=VSP_004614.
SQ   SEQUENCE   190 AA; 22310 MW; EDBF903E46E24789 CRC64;

Query Match   78.3%; Score 36; DB 1; Length 190;
Best Local Similarity   75.0%; Pred. No. 4.1;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
          || |||||
Db   86 CNDESLEC 93

RESULT 7
VEGD_MOUSE
ID   VEGD_MOUSE   STANDARD;   PRT;   358 AA.
AC   P97946;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF).
GN   FIGF OR VEGFD.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Fibroblast;
RX   MEDLINE=97030254; PubMed=8876195;
RA   Orlandini M., Marconcini L., Ferruzzi R., Oliviero S.;
RT   "Identification of a c-fos-induced gene that is related to the

RT   platelet-derived growth factor/vascular endothelial growth factor
RT   family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=97349118; PubMed=9205122;
RA   Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
RN   [3]
RP   DEVELOPMENTAL STAGE.
RX   MEDLINE=98288130; PubMed=9622638;
RA   Avantaggiato V., Orlandini M., Acampora D., Oliviero S., Simeone A.;
RT   "Embryonic expression pattern of the murine figf gene, a growth factor
RT   belonging to platelet-derived growth factor/vascular endothelial
RT   growth factor family.";
RL   Mech. Dev. 73:221-224(1998).
RN   [4]
RP   RECEPTOR SPECIFICITY.
RX   MEDLINE=21276411; PubMed=11279005;
RA   Baldwin M.E., Catimel B., Nice E.C., Roufail S., Hall N.E.,
RA   Stenvers K.L., Karkkainen M.J., Alitalo K., Stacker S.A., Achen M.G.;
RT   "The specificity of receptor binding by vascular endothelial growth
RT   factor-d is different in mouse and man.";
RL   J. Biol. Chem. 276:19166-19171(2001).
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC   and endothelial cell growth, stimulating their proliferation and
CC   migration and also has effects on the permeability of blood
CC   vessels. May function in the formation of the venous and lymphatic
CC   vascular systems during embryogenesis, and also in the maintenance
CC   of differentiated lymphatic endothelium in adults. Binds and
CC   activates VEGFR-3 (Flt4) receptor.
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in fetal and adult lung.
CC   -!- DEVELOPMENTAL STAGE: Expressed in a dynamic pattern in several
CC   body structures and organs of the embryo such as limb buds,
CC   acoustic ganglion, teeth, heart, anterior pituitary as well as
CC   lung and kidney mesenchyme, liver, derma, and periosteum of the
CC   vertebral column.
CC   -!- INDUCTION: By the transcription factor c-fos.
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC   variety of processed secreted forms with increased activity toward
CC   VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC   linked by disulfide bonds before secretion. The fully processed
CC   VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC   bound by non-covalent interactions (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   ---
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; X99572; CAA67892.1; -.
DR   EMBL; D89628; BAA14002.1; -.
DR   HSSP; P15692; 1VPP.
DR   PMMA-2DPAGE; P97946; -.
DR   MGD; MGI:108037; Figf.
DR   GO; GO:0005576; C:extracellular; IDA.
DR   GO; GO:0008083; F:growth factor activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0008283; P:cell proliferation; IDA.
DR   InterPro; IPR004153; CXCXC repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 2.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.

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DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS00278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL     1     21    POTENTIAL.
FT   PROPEP    22     93    POTENTIAL.
FT   CHAIN     94    210    VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP   211    358    POTENTIAL.
FT   DOMAIN   227    323    4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT                          X(1,3)-C.
FT   REPEAT   227    242    1 (APPROXIMATE).
FT   REPEAT   263    278    2.
FT   REPEAT   282    298    3.
FT   REPEAT   306    323    4.
FT   DISULFID 116    158    BY SIMILARITY.
FT   DISULFID 147    194    BY SIMILARITY.
FT   DISULFID 151    196    BY SIMILARITY.
FT   DISULFID 141    141    INTERCHAIN (BY SIMILARITY).
FT   DISULFID 150    150    INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD 160    160    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD 190    190    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD 292    292    N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE 358 AA;  40908 MW;  6636B17BF07037C CRC64;

Query Match   78.3%;  Score 36;  DB 1;  Length 358;
Best Local Similarity   62.5%;  Pred. No. 8;
Matches    5;  Conservative   2;  Mismatches   2;  Indels   1;  Gaps   0;

Qy     1  CNEESLIC 8
          ||||.::|
Db   151  CNEEGVMC 158

RESULT 8
FASC_STRPU
ID   FASC_STRPU   STANDARD;   PRT;   495 AA.
AC   Q05634;
DT   01-NOV-1997 (Rel. 35, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fascin.
OS   Strongylocentrotus purpuratus (Purple sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC   Strongylocentrotus.
OX   NCBI_TaxID=7668;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94022326; PubMed=8415664;
RA   Bryan J., Edwards R.H., Matsudaira P., Otto J., Wulfkuhle J.;
RT   "Fascin, an echinoid actin-bundling protein, is a homolog of the
RT   Drosophila singed gene product.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:9115-9119(1993).
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=79051184; PubMed=731692;
RA   Bryan J., Kane R.E.;
RT   "Separation and interaction of the major components of sea urchin
RT   actin gel.";
RL   J. Mol. Biol. 125:207-224(1978).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=77051438; PubMed=1033188;
RA   Kane R.E.;
RT   "Actin polymerization and interaction with other proteins in
RT   temperature-induced gelation of sea urchin egg extracts.";
RL   J. Cell Biol. 71:704-714(1976).
CC   -!- FUNCTION: ACTS AS AN ACTIN BUNDLING PROTEIN.
CC   -!- SIMILARITY: Belongs to the fascin family.
CC   --------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------
DR   EMBL; L12047; AAC37183.1; -.
DR   InterPro; IPR008999; Actin_crosslink.
KW   Actin-binding.
FT   INIT_MET   0      0
SQ   SEQUENCE 495 AA;  54813 MW;  D3B0B5CC52C21593 CRC64;

Query Match   76.1%;  Score 35;  DB 1;  Length 495;
Best Local Similarity   75.0%;  Pred. No. 18;
Matches    6;  Conservative   0;  Mismatches   0;  Indels   2;  Gaps   0;

Qy     1  CNEESLIC 8
          ||||||||
Db   108  CNGEELIC 115

RESULT 9
PKSL_BACSU
ID   PKSL_BACSU   STANDARD;   PRT;   4427 AA.
AC   Q05470;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Putative polyketide synthase pksL (PKS).
GN   PKSL OR PKSX OR PKSA OR OUTG OR BSU17190.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168 / PB1424;
RX   MEDLINE=93345824; PubMed=8344529;
RA   Scotti C., Piatti M., Cuzzoni A., Perani P., Tognoni A., Grandi G.,
RA   Galizzi A., Albertini A.M.;
RT   "A Bacillus subtilis large ORF coding for a polypeptide highly
RT   similar to polyketide synthases.";
RL   Gene 130:65-71(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA   Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA   Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA   Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA   Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA   Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA   Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA   Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA   Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA   Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA   Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA   Sekiguchi J., Sekowska A., Seror S.J., Serror S.J., Shin B.S., Soldo B.,
RA   Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA   Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA   Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA   Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA   Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
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RA   Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
RN   [3]
RP   SEQUENCE OF 3619-4427 FROM N.A.
RC   STRAIN=168 / PB1424;
RA   Grandi G.;
RL   Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: POTENTIALLY INVOLVED IN SOME INTERMEDIATE STEPS FOR
CC       THE SYNTHESIS OF A POLYKETIDE MOLECULE WHICH MAY BE INVOLVED IN
CC       SECONDARY METABOLISM.
CC   -!- COFACTOR: Contains 5 covalently bound phosphopantetheines
CC       (Potential).
CC   -!- SIMILARITY: Contains 5 acyl carrier domains.
CC
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; Z14098; CAA78479.1; -.
DR   EMBL; U11039; AAA85145.1; -.
DR   EMBL; Z99113; CAB13602.1; -.
DR   EMBL; Z35133; CAB84504.1; -.
DR   PIR; S25021; PN0637.
DR   SubtiList; BG10698; pksL.
DR   InterPro; IPR002198; ADH_short.
DR   InterPro; IPR000794; Ketoacyl_synth.
DR   InterPro; IPR006163; Pp_bind.
DR   InterPro; IPR006162; Ppantne_S.
DR   Pfam; PF00106; adh_short; 1.
DR   Pfam; PF00109; ketoacyl-synt; 4.
DR   Pfam; PF02801; ketoacyl-synt_C; 4.
DR   Pfam; PF00550; pp-binding; 5.
DR   PROSITE; PS00012; PHOSPHOPANTETHEINE; 5.
DR   PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR   PROSITE; PS50075; ACP_DOMAIN; 5.
KW   Transferase; Acyltransferase; Antibiotic biosynthesis; NADP;
KW   Phosphopantetheine; Multifunctional enzyme; Repeat; Complete proteome.
FT   DOMAIN    211    280  ACYL CARRIER (ACP) 1.
FT   DOMAIN    382    759  BETA-KETOACYL SYNTHASE 1.
FT   DOMAIN    937   1115  DEHYDRATASE.
FT   DOMAIN   1409   1602  BETA-KETOACYL REDUCTASE 1.
FT   DOMAIN   1687   1759  ACYL CARRIER (ACP) 2.
FT   DOMAIN   1876   2253  BETA-KETOACYL SYNTHASE 2.
FT   DOMAIN   2491   2560  ACYL CARRIER (ACP) 3.
FT   DOMAIN   2632   2701  ACYL CARRIER (ACP) 4.
FT   DOMAIN   2823   3182  BETA-KETOACYL SYNTHASE 3.
FT   DOMAIN   3575   3776  BETA-KETOACYL REDUCTASE 2.
FT   DOMAIN   3854   3923  ACYL CARRIER (ACP) 5.
FT   DOMAIN   4019   4373  BETA-KETOACYL SYNTHASE 4.
FT   BINDING   243    243  PHOSPHOPANTETHEINE (POTENTIAL).
FT   BINDING  1723   1723  PHOSPHOPANTETHEINE (POTENTIAL).
FT   BINDING  2523   2523  PHOSPHOPANTETHEINE (POTENTIAL).
FT   BINDING  2664   2664  PHOSPHOPANTETHEINE (POTENTIAL).
FT   BINDING  3886   3886  PHOSPHOPANTETHEINE (POTENTIAL).
SQ   SEQUENCE   4427 AA;  493398 MW;  9612521E561AB9F2 CRC64;

Query Match  76.1%;  Score 35;  DB 1;  Length 4427;
Best Local Similarity  62.5%;  Pred. No. 1.7e+02;
Matches   5;  Conservative   1;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      1 CNEESLIC 8
            |||| :|
Db   1205 CNEEGQVC 1212

RESULT 10
N189_SCHPO
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ID   N189_SCHPO     STANDARD;      PRT;   1778 AA.
AC   Q9UTK4; P78796;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Nucleoporin nup189 (Nuclear pore protein nup189).
GN   NUP189 OR SPAC1486.05.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
RN   [2]
RP   SEQUENCE OF 1428-1778 FROM N.A.
RC   STRAIN=PR745;
RX   MEDLINE=98162722; PubMed=9501991;
RA   Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
RT   "Identification of open reading frames in Schizosaccharomyces pombe
RT   cDNAs.";
RL   DNA Res. 4:363-369(1997).
RN   [3]
RP   IDENTIFICATION, AND SUBUNIT.
RX   MEDLINE=22263608; PubMed=12376568;
RA   Tange Y., Hirata A., Niwa O.;
RT   "An evolutionarily conserved fission yeast protein, Ned1, implicated
RT   in normal nuclear morphology and chromosome stability, interacts with
RT   Dis3, Piml/RCC1 and an essential nucleoporin.";
RL   J. Cell Sci. 115:4375-4385(2002).
CC   -!- SUBUNIT: Monomer. Interacts with ned1.
CC   -!- SUBCELLULAR LOCATION: Nuclear pore complex (By similarity).
CC   -!- DOMAIN: Contains G-L-F-G repeats.
CC   -!- SIMILARITY: Belongs to the GLFG family of nucleoporins.
CC
CC   --------------------------------------------------------------------------
```
```
CC   --------------------------------------------------------------------------
DR   EMBL; AL133357; CAB62415.1; -.
DR   EMBL; D89145; BAA13807.1; -.
```

DR   PIR; T50074; T50074.
DR   HSSP; P22629; 1SWF.
DR   GeneDB_SPombe; SPAC1486.05; -.
DR   GO; GO:0016020; C:membrane; ISS.
DR   GO; GO:0005643; C:nuclear pore; ISS.
DR   GO; GO:0006606; P:protein-nucleus import; ISS.
DR   InterPro; IPR007230; Nucleoporin_FG.
DR   InterPro; IPR004325; Nucleoporin_FG.
DR   Pfam; PF04096; Nucleoporin2; 1.
DR   Pfam; PF03093; Nucleoporin_FG; 24.
KW   Nuclear protein; Transport; Repeat.
FT   DOMAIN   9   625   GLY-RICH.
FT   DOMAIN   233   596   THR-RICH.
FT   DOMAIN   393   442   ASN-RICH.
SQ   SEQUENCE   1778 AA;   189575 MW;   1D2AED57D927ADC6 CRC64;

Query Match   75.0%; Score 34.5; DB 1; Length 1778;
Best Local Similarity   72.7%; Pred. No. 84;
Matches   8; Conservative   0; Mismatches   0; Indels   3; Gaps   1;

Qy   1 CNEESL---IC 8
               | ||||| ||
Db   1748 CNEESITDAIC 1758

RESULT 11
CPJ1_RABIT
ID   CPJ1_RABIT   STANDARD;   PRT;   500 AA.
AC   P52786;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cytochrome P450 2J1 (EC 1.14.14.1) (CYPIIJ1) (P-450IB).
GN   CYP2J1.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=92011499; PubMed=1717443;
RA   Kikuta Y., Sogawa K., Haniu M., Kinosaki M., Kusunose E., Nojima Y.,
RA   Yamamoto S., Ichihara K., Kusunose M., Fujii-Kuriyama Y.;
RT   "A novel species of cytochrome P-450 (P-450ib) specific for the small
RT   intestine of rabbits. cDNA cloning and its expression in COS cells.";
RL   J. Biol. Chem. 266:17821-17825(1991).
CC   -!- FUNCTION: CATALYZES THE N-DEMETHYLATION OF BENZPHETAMINE TO
CC   FORMALDEHYDE.
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC   oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- TISSUE SPECIFICITY: SMALL INTESTINE.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   --
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; D90405; BAA14401.1; -.
DR   PIR; A40938; A40938.
DR   HSSP; P00179; 1DT6.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR008071; EP450_CYP2J.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR01688; EP450ICYP2J.
DR   PRINTS; PR01688; EP450ICYP2J.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW   Microsome; Endoplasmic reticulum.

FT   INIT_MET   0   0
FT   METAL   446   446   IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ   SEQUENCE   500 AA;   57194 MW;   A0EEE62B5FF23DE CRC64;

Query Match   73.9%; Score 34; DB 1; Length 500;
Best Local Similarity   85.7%; Pred. No. 28;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   2 NEESLIC 8
               ||:|:|||
Db   296 NEENLIC 302

RESULT 12
CPJ6_MOUSE
ID   CPJ6_MOUSE   STANDARD;   PRT;   501 AA.
AC   O54750;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cytochrome P450 2J6 (EC 1.14.14.1) (CYPIIJ6) (Arachidonic acid
DE   epoxygenase).
GN   CYP2J6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX   MEDLINE=98234557; PubMed=9570962;
RA   Ma J., Ramachandran S., Fiedorek F.T. Jr., Zeldin D.C.;
RT   "Mapping of the CYP2J cytochrome P450 genes to human chromosome 1 and
RT   mouse chromosome 4.";
RL   Genomics 49:152-155(1998).
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC   oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   --
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CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; U62295; AAB87636.1; -.
DR   HSSP; P00179; 1DT6.
DR   MGD; MGI:1270148; Cyp2j6.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR008071; EP450_CYP2J.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR01688; EP450ICYP2J.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW   Microsome; Endoplasmic reticulum.
FT   METAL   447   447   IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ   SEQUENCE   501 AA;   57820 MW;   4E5A26B35D831E37 CRC64;

Query Match   73.9%; Score 34; DB 1; Length 501;
Best Local Similarity   85.7%; Pred. No. 28;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   2 NEESLIC 8
               ||:|:|||
Db   296 NEENLIC 302

RESULT 13
CPJ3_RAT

```
ID   CPJ3_RAT       STANDARD;      PRT;   502 AA.
AC   P51590;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cytochrome P450 2J3 (EC 1.14.14.1) (CYPIIJ3).
GN   CYP2J3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Fischer 344;
RX   MEDLINE=97284730; PubMed=9139707;
RA   Wu S., Chen W., Murphy E., Gabel S., Tomer K.B., Foley J.,
RA   Steenbergen C., Falck J.R., Moomaw C.R., Zeldin D.C.;
RT   "Molecular cloning, expression, and functional significance of a
RT   cytochrome P450 highly expressed in rat heart myocytes.";
RL   J. Biol. Chem. 272:12551-12559(1997).
CC   -!- FUNCTION: THIS ENZYME METABOLIZES ARACHIDONIC ACID PREDOMINANTLY
CC       VIA A NADPH-DEPENDENT OLEFIN EPOXIDATION MAINLY TO 14,15-, 11,12-,
CC       AND 8,9-EPOXYEICOSATRIENOIC ACIDS (EET). IT ALSO ACTS AS AN OMEGA-
CC       1-HYDROXYLASE BY METABOLIZING ARACHIDONIC ACID TO 19-
CC       HYDROXYEICOSATETRAENOIC ACID (19-OH-AA).
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC       oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART AND LIVER.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; U39943; AAB48545.1; -.
DR   HSSP; P00179; 1DT6.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR0008071; EP450_CYP2J.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR01688; EP450ICYP2J.
DR   PRINTS; PR01685; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW   Microsome; Endoplasmic reticulum; NADP.
FT   METAL       448    448   IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ   SEQUENCE   502 AA;   57969 MW;   CCC0AE67977FFF31 CRC64;

Query Match     73.9%;   Score 34;   DB 1;   Length 502;
Best Local Similarity   85.7%;   Pred. No. 28;
Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    2 NEESLIC 8
          |||:|||
Db  297 NEENLIC 303

RESULT 14
LGI2_HUMAN
ID   LGI2_HUMAN     STANDARD;      PRT;   545 AA.
AC   Q8NOV4; Q8NDW6; Q96PX2;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Leucine-rich repeat LGI family member 2 precursor (Leucine-rich
DE   glioma-inactivated protein 2) (LGI1-like protein 2).
GN   LGI2 OR LGI1L OR KIAA1916.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22017856; PubMed=12023020;
RA   Gu W., Wevers A., Schroder H., Grzeschik K.H., Derst C., Brodtkorb E.,
RA   de Vos R., Steinlein O.K.;
RT   "The LGI1 gene involved in lateral temporal lobe epilepsy belongs to a
RT   new subfamily of leucine-rich repeat proteins.";
RL   FEBS Lett. 519:71-76(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22090568; PubMed=12095917;
RA   Scheel H., Tomiuk S., Hofmann K.;
RT   "A common protein interaction domain links two recently identified
RT   epilepsy genes.";
RL   Hum. Mol. Genet. 11:1757-1762(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22207944; PubMed=12217514;
RA   Staub E., Perez-Tur J., Siebert R., Nobile C., Moschonas N.K.,
RA   Deloukas P., Hinzmann B.;
RT   "The novel EPTP repeat defines a superfamily of proteins implicated in
RT   epileptic disorders.";
RL   Trends Biochem. Sci. 27:441-444(2002).
RN   [4]
RP   SEQUENCE OF 4-545 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21456161; PubMed=11572484;
RA   Nagase T., Kikuno R., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XXI.
RT   The complete sequences of 60 new cDNA clones from brain which code for
RT   large proteins.";
RL   DNA Res. 8:179-187(2001).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- SIMILARITY: Contains 5 EAR repeats.
CC   -!- SIMILARITY: Contains 4 leucine-rich (LRR) repeats.
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; AF467955; AAM49553.1; -.
DR   EMBL; AJ487958; CAD32305.1; -.
DR   EMBL; AJ487516; CAD31784.1; -.
DR   EMBL; AB067503; BAB67809.1; -.
DR   Genew; HGNC:18710; LGI2.
DR   InterPro; IPR009039; EAR.
DR   InterPro; IPR005492; EPTP.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF03736; EPTP; 2.
DR   Pfam; PF00560; LRR; 3.
DR   Pfam; PF01463; LRRCT; 1.
DR   SMART; SM00369; LRR_TYP; 3.
DR   SMART; SM00082; LRRCT; 1.
DR   PROSITE; PS50912; EAR; 5.
KW   Repeat; Leucine-rich repeat; Signal.
FT   SIGNAL        1     28   POTENTIAL.
FT   CHAIN        29    545   LEUCINE-RICH REPEAT LGI FAMILY MEMBER 2.
FT   REPEAT       60     83   LRR 1.
FT   REPEAT       84    107   LRR 2.
FT   REPEAT      109    131   LRR 3.
FT   REPEAT      132    155   LRR 4.
FT   REPEAT      218    261   EAR 1.
FT   REPEAT      310    358   EAR 2.
FT   REPEAT      359    403   EAR 3.
FT   REPEAT      406    450   EAR 4.
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FT   REPEAT      451    494       EAR 5.
FT   CARBOHYD     70     70       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    271    271       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    402    402       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    524    524       F -> L (IN REF. 2 AND 4).
SQ   SEQUENCE    545 AA;   62298 MW;   FD29B51F01B3D7E2 CRC64;

Query Match                  73.9%;   Score 34;   DB 1;   Length 545;
Best Local Similarity   62.5%;   Pred. No. 31;
Matches     5;   Conservative    2;   Mismatches    1;   Indels    0;   Gaps    0;

Qy       1  CNEESLIC 8
            | :|:|:||
Db      42  CTKESIIC 49


RESULT 15
LGI2_MOUSE
ID   LGI2_MOUSE     STANDARD;     PRT;     550 AA.
AC   Q8K4Z0; Q80T76;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Leucine-rich repeat LGI family member 2 precursor (Leucine-rich
DE   glioma-inactivated protein 2).
GN   LGI2 OR KIAA1916.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=C57BL/6J;
RX   MEDLINE=22207944; PubMed=12217514;
RA   Staub E., Perez-Tur J., Siebert R., Nobile C., Moschonas N.K.,
RA   Deloukas P., Hinzmann B.;
RT   "The novel EPTP repeat defines a superfamily of proteins implicated in
RT   epileptic disorders.";
RL   Trends Biochem. Sci. 27:441-444(2002).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=22579291; PubMed=12693553;
RA   Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA   Nakajima D., Nagase T., Ohara O., Koga H.;
RT   "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT   II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT   cDNAs identified by screening of terminal sequences of cDNA clones
RT   randomly sampled from size-fractionated libraries.";
RL   DNA Res. 10:35-48(2003).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q8K4Z0-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q8K4Z0-2; Sequence=VSP_007680, VSP_007681;
CC   -!- SIMILARITY: Contains 5 EAR repeats.
CC   -!- SIMILARITY: Contains 4 leucine-rich (LRR) repeats.
CC   -------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; AJ487515; CAD31783.1; -.
DR   EMBL; AK122570; BAC65852.1; ALT_INIT.
DR   MGD; MGI:2180196; Lgi2.
DR   InterPro; IPR009039; EAR.
DR   InterPro; IPR005492; EPTP.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF03736; EPTP; 2.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   SMART; SM00369; LRR_TYP; 2.
DR   SMART; SM00082; LRRCT; 1.
DR   PROSITE; PS50912; EAR; 5.
KW   Repeat; Leucine-rich repeat; Signal; Alternative splicing.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    550       LEUCINE-RICH REPEAT LGI FAMILY MEMBER 2.
FT   REPEAT       57     80       LRR 1.
FT   REPEAT       81    104       LRR 2.
FT   REPEAT      106    128       LRR 3.
FT   REPEAT      130    152       LRR 4.
FT   REPEAT      223    266       EAR 1.
FT   REPEAT      315    363       EAR 2.
FT   REPEAT      364    408       EAR 3.
FT   REPEAT      411    455       EAR 4.
FT   REPEAT      456    499       EAR 5.
FT   CARBOHYD     67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    159    159       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    276    276       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    407    407       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    135    135       L -> LSLANNHIKALPRDVFSDLDSLIEL (in
FT                                isoform 2).
FT                                /FTId=VSP_007680.
FT   VARSPLIC    192    223       Missing (in isoform 2).
FT                                /FTId=VSP_007681.
SQ   SEQUENCE    550 AA;   63006 MW;   56974B9DE663CCD1 CRC64;

Query Match                  73.9%;   Score 34;   DB 1;   Length 550;
Best Local Similarity   62.5%;   Pred. No. 31;
Matches     5;   Conservative    2;   Mismatches    1;   Indels    0;   Gaps    0;

Qy       1  CNEESLIC 8
            | :|:|:||
Db      39  CTKESIIC 46


Search completed: September 5, 2004, 09:56:02
Job time : 4.63636 secs
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              GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:      September 5, 2004, 09:46:09 ; Search time 18.101 Seconds
                                           (without alignments)
                                           139.448 Million cell updates/sec

Title:       US-09-761-636A-6
Perfect score: 46
Sequence:    1 CNEESLIC 8
Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    1017041 seqs, 31518202 residues

Total number of hits satisfying chosen parameters:   1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_25:*
        1:  sp_archea:*
        2:  sp_bacteria:*
        3:  sp_fungi:*
        4:  sp_human:*
        5:  sp_invertebrate:*
        6:  sp_mammal:*
        7:  sp_mhc:*
        8:  sp_organelle:*
        9:  sp_phage:*
       10:  sp_plant:*
       11:  sp_rodent:*
       12:  sp_virus:*
       13:  sp_vertebrate:*
       14:  sp_unclassified.*
       15:  sp_rvirus:*
       16:  sp_bacteriap:*
       17:  sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	40	87.0	252	13	Q8QGD7	Q8qgd7 gallus gall
2	40	87.0	326	11	Q91ZE4	Q91ze4 rattus norv
3	37	80.4	152	12	Q8B571	Q8b571 pseudocowpo
4	37	80.4	200	16	Q81XN1	Q81xn1 bacillus an
5	36	78.3	65	6	Q8MIN0	Q8min0 capra hircu
6	36	78.3	68	6	Q97500	Q97500 oryctolagus
7	36	78.3	75	6	O18843	O18843 oryctolagus
8	36	78.3	78	6	Q9NIS2	Q9nis2 capreolus c
9	36	78.3	109	6	Q8MIN1	Q8min1 capra hircu
10	36	78.3	118	6	Q9MZB1	Q9mzb1 ovis aries
11	36	78.3	120	6	Q866G4	Q866g4 oryctolagus
12	36	78.3	123	6	Q9N1S1	Q9n1s1 capreolus c
13	36	78.3	131	6	Q8MJ86	Q8mj86 capreolus c
14	36	78.3	132	12	Q9YMF3	Q9ymf3 orf virus.
15	36	78.3	136	12	Q80GE8	Q80ge8 orf virus.
16	36	78.3	148	13	O42571	O42571 xenopus lae
17	36	78.3	190	6	O77643	O77643 ovis aries
18	36	78.3	194	13	O42572	O42572 xenopus lae
19	36	78.3	267	2	Q8VU11	Q8vu11 bacteroides
20	36	78.3	421	5	Q95T10	Q95t10 drosophila
21	36	78.3	502	5	Q9VFF4	Q9vff4 drosophila
22	36	78.3	864	4	Q8IZZ3	Q8izz3 homo sapien
23	36	78.3	1115	5	Q27764	Q27764 plasmodium
24	36	78.3	1778	5	Q96JI4	Q96ji4 homo sapien
25	35	76.1	83	16	Q81RL5	Q81rl5 bacillus an
26	35	76.1	227	4	Q891A7	Q891a7 clostridium
27	35	76.1	435	8	Q8N5U8	Q8n5u8 homo sapien
28	35	76.1	837	13	Q7T1T7	Q7t1t7 fugu rubrip
29	35	76.1	1062	13	Q7ZUM7	Q7zum7 brachydanio
30	34	73.9	148	11	Q8K1C5	Q8k1c5 mus musculu
31	34	73.9	241	2	Q93FQ7	Q93fq7 cowdria rum
32	34	73.9	295	17	O58637	O58637 pyrococcus
33	34	73.9	317	5	Q9W1E4	Q9w1e4 drosophila
34	34	73.9	365	12	Q8B590	Q8b590 choristoneu
35	34	73.9	374	11	Q91W71	Q91w71 mus musculu
36	34	73.9	435	11	Q9VSV3	Q9vsv3 drosophila
37	34	73.9	435	5	Q8MSL3	Q8msl3 drosophila
38	34	73.9	501	5	Q9QXF7	Q9qxf7 rattus norv
39	34	73.9	501	11	Q8BR78	Q8br78 mus musculu
40	34	73.9	502	11	Q924D1	Q924d1 mus musculu
41	34	73.9	529	11	Q9CRQ9	Q9crq9 mus musculu
42	34	73.9	642	10	Q9LER1	Q9ler1 arabidopsis
43	34	73.9	838	5	Q9VQA9	Q9vqa9 drosophila
44	34	73.9	1102	4	Q86XZ1	Q86xz1 homo sapien
45	34	73.9	1712	5	Q8ICW9	Q8icw9 plasmodium

ALIGNMENTS

```
RESULT 1
Q8QGD7
ID   Q8QGD7        PRELIMINARY;       PRT;   252 AA.
AC   Q8QGD7;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor D.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Diaz-Trelles R., Rodriguez-Leon J., Kawakami Y.,
RA   Izpisua-Belmonte J.C.;
RT   "Expression of the chick vascular endothelial growth factor D gene
RT   during limb development.";
RL   Mech. Dev. 0:0-0(2002).
DR   EMBL; AF479650; AAM12733.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   252 AA;  28767 MW;  643475DAB2E72F27 CRC64;

Query Match             87.0%;  Score 40;  DB 13;  Length 252;
Best Local Similarity   87.5%;  Pred. No. 1.8;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1  CNEESLIC 8
           |||||| |
Db    146  CNEESLSC 153
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DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   152 AA;   16202 MW;   F4B3956D60B37A3D CRC64;

Query Match             80.4%;   Score 37;  DB 12;  Length 152;
Best Local Similarity   75.0%;   Pred. No. 4.9;
Matches      6;  Conservative   1;  Mismatches  1;  Indels  0;  Gaps  0;

Qy       1 CNEESLIC 8
           ||:||:||
Db      89 CNDESQIC 96

RESULT 4
Q81XN1
ID   Q81XN1              PRELIMINARY;      PRT;    200 AA.
AC   Q81XN1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   BA5202.
OS   Bacillus anthracis (strain Ames).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=198094;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22608414; PubMed=12721629;
RA   Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA   Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA   Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA   Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA   DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA   Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune J.,
RA   Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA   Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA   Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA   Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA   Fraser C.M.;
RT   "The genome sequence of Bacillus anthracis Ames and comparison to
RT   closely related bacteria.";
RL   Nature 423:81-86(2003).
DR   EMBL; AE017040; AAP28871.1; -.
DR   TIGR; BA5202; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   200 AA;   23905 MW;   70E8DD90E5DBA7A0 CRC64;

Query Match             80.4%;   Score 37;  DB 16;  Length 200;
Best Local Similarity   62.5%;   Pred. No. 6.3;
Matches      5;  Conservative   2;  Mismatches  2;  Indels  1;  Gaps  0;

Qy       1 CNEESLIC 8
           ||:|:||
Db      52 CNDEKMIC 59

RESULT 5
Q8MIN0
ID   Q8MIN0              PRELIMINARY;      PRT;     65 AA.
AC   Q8MIN0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   vascular endothelial growth factor 121 (Fragment).
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Corpus luteum;
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RESULT 2
Q91ZE4
ID   Q91ZE4              PRELIMINARY;      PRT;    326 AA.
AC   Q91ZE4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   VEGF-D.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,
RA   Pepper M.S., Giannis A., Sleeman J.P.;
RT   "Characterization of indolinones which specifically inhibit VEGF-C and
RT   VEGF-D-induced activation of VEGFR-3 but not VEGFR-2.";
RL   Eur. J. Biochem. 0:0-0(2001).
DR   EMBL; AY032728; AAK96008.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 1.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   326 AA;   37106 MW;   D7CAEBA6C9FABB7D CRC64;

Query Match             87.0%;   Score 40;  DB 11;  Length 326;
Best Local Similarity   75.0%;   Pred. No. 2.3;
Matches      6;  Conservative   2;  Mismatches  2;  Indels  0;  Gaps  0;

Qy       1 CNEESLIC 8
           ||||||:||
Db     151 CNEESVMC 158

RESULT 3
Q8B571
ID   Q8B571              PRELIMINARY;      PRT;    152 AA.
AC   Q8B571;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vascular endothelial growth factor-like protein.
GN   VEGF.
OS   Pseudocowpox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=129726;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VR634;
RA   Ueda N., Wise L.M., Stacker S.A., Fleming S.B., Mercer A.A.;
RT   "Pseudocowpox virus encodes a homolog of vascular endothelial growth
RT   factor.";
RL   Virology 0:0-0(2003).
DR   EMBL; AF542070; AAO16216.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
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RA   Kawate N., Tsuji M., Tamada H., Inaba T., Sawada T.;
RT   "Changes of Messenger RNAs Encoding Vascular Endothelial Growth Factor
RT   and Its Receptors during the Development and Maintenance of Caprine
RT   Corpora Lutea.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY114353; AAM76674.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER   1   1
SQ   SEQUENCE   65 AA; 7562 MW; BA3E5384364B05E3 CRC64;

Query Match   78.3%; Score 36; DB 6; Length 65;
Best Local Similarity   75.0%; Pred. No. 3.6;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
              |:|||:|
Db   5 CNDESLEC 12

RESULT 6
097500
ID   097500   PRELIMINARY;   PRT;   68 AA.
AC   097500;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor (Fragment).
GN   VEGF.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Inoue K., Kawabe Y., Kodama T.;
RT   "Rabbit VEGF cDNA,partial.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB020216; BAA36649.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER   1   1
FT   NON_TER   68   68
SQ   SEQUENCE   68 AA; 7819 MW; 68763866IB98DEE0 CRC64;

Query Match   78.3%; Score 36; DB 6; Length 68;
Best Local Similarity   75.0%; Pred. No. 3.8;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
              |:|||:|
Db   41 CNDESLEC 48

RESULT 7
018843
ID   018843   PRELIMINARY;   PRT;   75 AA.
AC   018843;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)

DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor (Fragment).
GN   VEGF.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NEW ZEALAND WHITE; TISSUE=Skeletal muscle;
RX   MEDLINE=98191144; PubMed=9530113;
RA   Skorjanc D., Jaschinski F., Heine G., Pette D.;
RT   "Sequential increases in capillarization and mitochondrial enzymes in
RT   low-frequency-stimulated rabbit muscle.";
RL   Am. J. Physiol. 274:C810-C818(1998).
DR   EMBL; AF022179; AAC15469.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER   1   1
FT   NON_TER   75   75
SQ   SEQUENCE   75 AA; 8720 MW; DDCE2C5B29E69359 CRC64;

Query Match   78.3%; Score 36; DB 6; Length 75;
Best Local Similarity   75.0%; Pred. No. 4.1;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
              |:|||:|
Db   29 CNDESLEC 36

RESULT 8
Q9N1S2
ID   Q9N1S2   PRELIMINARY;   PRT;   78 AA.
AC   Q9N1S2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor isoform 121 (Fragment).
GN   VEGF.
OS   Capreolus capreolus (Roe deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Capreolus.
OX   NCBI_TaxID=9858;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=20532861; PubMed=11078967;
RA   Wagener A., Blotner S., Goritz F., Fickel J.;
RT   "Detection of growth factors in the testis of roe deer (Capreolus
RT   capreolus).";
RL   Anim. Reprod. Sci. 54:65-75(2000).
DR   EMBL; AF152593; AAF73232.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.

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DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER      1      1
FT   NON_TER     78     78
SQ   SEQUENCE   78 AA;  9131 MW;  7EE20DDFFC17847C CRC64;

Query Match                78.3%;
Best Local Similarity      75.0%;
Matches    6;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy      1 CNEESLIC 8
            ||:||| |
Db     25 CNDESLEC 32

RESULT 9
Q8MIN1
ID   Q8MIN1;         PRELIMINARY;        PRT;    109 AA.
AC   Q8MIN1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelia growth factor 165 (Fragment).
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Corpus luteum;
RA   Kawate N., Tsuji M., Tamada H., Inaba T., Sawada T.;
RT   "Changes of Messenger RNAs Encoding Vascular Endothelial Growth Factor
RT   and Its Receptors during the Development and Maintenance of Caprine
RT   Corpora Lutea.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY114352; AAM76673.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER      1      1
SQ   SEQUENCE  109 AA;  12656 MW;  91265725lA37E023 CRC64;

Query Match                78.3%;
Best Local Similarity      75.0%;
Matches    6;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy      1 CNEESLIC 8
            ||:||| |
Db      5 CNDESLEC 12

RESULT 10
Q9MZB1
ID   Q9MZB1;         PRELIMINARY;        PRT;    118 AA.
AC   Q9MZB1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor (Fragment).
GN   VEGF.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;

RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placental artery endothelium;
RA   Zheng J., Tsoi S.C., Magness R.R.;
RT   "Growth factor expression in ovine fetal placental artery endothelial
RT   cells.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF250375; AAF75258.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER      1      1
SQ   SEQUENCE  118 AA;  13931 MW;  757DC53AA56378A6 CRC64;

Query Match                78.3%;
Best Local Similarity      75.0%;
Matches    6;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy      1 CNEESLIC 8
            ||:||| |
Db     58 CNDESLEC 65

RESULT 11
Q866G4
ID   Q866G4;         PRELIMINARY;        PRT;    120 AA.
AC   Q866G4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vascular endothelial growth factor (Fragment).
GN   VEGF.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clausen I., Kietz S., Fischer B.;
RT   "Transcriptional changes in rabbit preimplantation blastocysts upon
RT   exposure to polychlorinated biphenyls.";
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY197796; AAO42518.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER      1      1
FT   NON_TER    120    120
SQ   SEQUENCE  120 AA;  14032 MW;  E563C54980DCE1E8 CRC64;

Query Match                78.3%;
Best Local Similarity      75.0%;
Matches    6;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy      1 CNEESLIC 8
            ||:||| |
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```
Db    74 CNDESLEC 81

RESULT 12
Q9N1S1
ID   Q9N1S1;            PRELIMINARY;      PRT;    123 AA.
AC   Q9N1S1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor isoform 165 (Fragment).
GN   VEGF.
OS   Capreolus capreolus (Roe deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Capreolus.
OX   NCBI_TaxID=9858;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=20532861; PubMed=11078967;
RA   Wagener A., Blotner S., Goritz F., Fickel J.;
RT   "Detection of growth factors in the testis of roe deer (Capreolus
RT   capreolus).";
RL   Anim. Reprod. Sci. 64:65-75(2000).
DR   EMBL; AF152594; AAF73233.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER      1      1
FT   NON_TER    123    123
SQ   SEQUENCE  123 AA;  14354 MW;  0A756F54105A4CE1 CRC64;

Query Match             78.3%;  Score 36;  DB 6;  Length 123;
Best Local Similarity   75.0%;  Pred. No. 6.6;
Matches    6;  Conservative    1;  Mismatches   1;  Indels   1;  Gaps   0;

Qy       1 CNEESLIC 8
           ||:||||
Db      25 CNDESLEC 32

RESULT 13
Q8MJ86
ID   Q8MJ86;            PRELIMINARY;      PRT;    131 AA.
AC   Q8MJ86;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor-3 (Fragment).
OS   Capreolus capreolus (Roe deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Capreolus.
OX   NCBI_TaxID=9858;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Wagener A., Fickel J.;
RT   "Detection of VEGF in roe deer testis.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF514284; AAM49789.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER      1      1
FT   NON_TER    131    131
SQ   SEQUENCE  131 AA;  15358 MW;  9971A5BEEAC7FCA CRC64;

Query Match             78.3%;  Score 36;  DB 6;  Length 131;
Best Local Similarity   75.0%;  Pred. No. 7;
Matches    6;  Conservative    1;  Mismatches   1;  Indels   1;  Gaps   0;

Qy       1 CNEESLIC 8
           ||:||||
Db       3 CNDESLEC 10

RESULT 14
Q9YMF3
ID   Q9YMF3;            PRELIMINARY;      PRT;    132 AA.
AC   Q9YMF3;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor homolog Vegf-e (Vascular
DE   endothelial growth factor-like protein).
GN   VEGF-E.
OS   Orf virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=10258;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=D1701;
RX   MEDLINE=99107753; PubMed=9889193;
RA   Meyer M., Clauss M., Lepple-Wienhues A., Waltenberger J.,
RA   Augustin H.G., Ziche M., Lanz C., Buettner M., Rziha H.J., Dehio C.;
RT   "A novel vascular endothelial growth factor encoded by orf virus,
RT   VEGF-E, mediates angiogenesis via signalling through VEGFR-2 (KDR) but
RT   not VEGFR-1 (Flt-1) receptor tyrosine kinases.";
RL   EMBO J. 18:363-374(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=D1701;
RX   PubMed=12692275;
RA   Rziha H.-J., Bauer B., Adam K.-H., Rottgen M., Cottone R., Henkel M.,
RA   Dehio C., Buttner M.;
RT   "Relatedness and heterogeneity at the near-terminal end of the genome
RT   of a parapoxvirus bovis 1 strain (B177) compared with parapoxvirus
RT   ovis (Orf virus).";
RL   J. Gen. Virol. 84:1111-1116(2003).
DR   EMBL; AF106020; AAD03735.1; -.
DR   EMBL; AY186732; AAO31702.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE  132 AA;  14763 MW;  15F403A068B72926 CRC64;

Query Match             78.3%;  Score 36;  DB 12;  Length 132;
Best Local Similarity   75.0%;  Pred. No. 7;
Matches    6;  Conservative    1;  Mismatches   1;  Indels   1;  Gaps   0;
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Qy        1 CNEESLIC 8
            ||:|||||
Db       70 CNDESLEC 77


RESULT 15
Q80GE8
ID   Q80GE8        PRELIMINARY;      PRT;   136 AA.
AC   Q80GE8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VEGF-like protein.
OS   Orf virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=10258;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Orf-11;
RA   McInnes C.J., Wood A.R.;
RT   "A preliminary transcript map of the early genes of orf virus.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY236150; AAP03726.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_Cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE  136 AA;  15082 MW;  9768C9C42E6CB267 CRC64;

Query Match             78.3%;  Score 36;  DB 12;  Length 136;
Best Local Similarity   75.0%;  Pred. No. 7.2;
Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;


Qy        1 CNEESLIC 8
            ||:|||||
Db       71 CNDESLEC 78


Search completed: September  5, 2004, 09:59:54
Job time : 20.101 secs
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                GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    September  5, 2004, 09:37:49 ; Search time 26.2626 Seconds
                                         (without alignments)
                                         86.068 Million cell updates/sec

Title:          US-09-761-636a-6
Perfect score:  46
Sequence:       1 CNEESLIC 8
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:       1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters:    1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  A_Geneseq_29Jan04:*
         1: geneseqp1980s:*
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         4: geneseqp2001s:*
         5: geneseqp2002s:*
         6: geneseqp2002as:*
         7: geneseqp2003as:*
         8: geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	100.0	8	4	AAU04525	Aau04525 VEGF base
2	46	100.0	9	4	AAU04528	Aau04528 VEGF base
3	46	100.0	73	4	AAU04522	Aau04522 Human VEG
4	46	100.0	96	4	AAU04520	Aau04520 Human VEG
5	46	100.0	109	3	AAY23889	Aay23889 Human vas
6	46	100.0	109	6	AAB11931	Aab11931 Human tru
7	46	100.0	109	6	ABB84621	Abb84621 Human wil
8	46	100.0	287	2	ABG73779	Abg73779 Human NVR
9	46	100.0	325	2	AAW53240	Aaw53240 Homo sapi
10	46	100.0	325	4	AAY97572	Aay97572 Human VEG
11	46	100.0	354	2	AAW44293	Aaw44293 Human vas
12	46	100.0	354	2	AAW49036	Aaw49036 Human zve
13	46	100.0	354	3	AAW53241	Aaw53241 Homo sapi
14	46	100.0	354	3	AAB10649	Aab10649 Human VEG
15	46	100.0	354	3	AAY70750	Aay70750 Human VEG
16	46	100.0	354	3	AAY70983	Aay70983 Human pre
17	46	100.0	354	3	AAB29049	Aab29049 Human vas
18	46	100.0	354	4	AAB37606	Aab37606 Human VEG
19	46	100.0	354	4	AAY97573	Aay97573 Human VEG
20	46	100.0	354	4	AAU08441	Aau08441 Polypepti
21	46	100.0	354	4	ABG33055	Abg33055 Human vas
22	46	100.0	354	5	ABG32046	Abg32046 Human Flt
23	46	100.0	354	6	ABB84623	Abb84623 Human VEG
24	46	100.0	354	7	ADD08950	Add08950 Human VEG
25	43	93.5	8	4	AAU04539	Aau04539 VEGF base
26	42	91.3	8	4	AAU04541	Aau04541 VEGF base
27	41	89.1	8	4	AAU04538	Aau04538 VEGF base
28	41	89.1	9	4	AAU04552	Aau04552 VEGF base
29	41	89.1	9	4	ABG73750	Abg73750 Human VEG
30	40	87.0	109	6	AAU04553	Aau04553 VEGF base
31	40	87.0	326	2	AAW44296	Aaw44296 Rat vascu
32	39	84.8	354	4	AAU04540	Aau04540 VEGF base
33	39	84.8	620	2	AAB70685	Aab70685 Human vas
34	39	84.8	923	2	AAW14994	Aaw14994 Human c-F
35	37	80.4	101	2	ABG20904	Abg20904 Novel hum
36	36	78.3	101	2	AAW86229	Aaw86229 Poxvirus
37	36	78.3	106	2	AAW86228	Aaw86228 Poxvirus
38	36	78.3	110	5	AAM47933	Aam47933 Mouse VEG
39	36	78.3	111	2	AAW86227	Aaw86227 Poxvirus
40	36	78.3	116	2	AAW86226	Aaw86226 Poxvirus
41	36	78.3	120	2	AAR10916	Aar10916 Bovine va
42	36	78.3	120	2	AAR38916	Aar38916 Bovine VE
43	36	78.3	132	2	AAW40305	Aaw40305 Parapox v
44	36	78.3	132	2	AAY33434	Aay33434 Parapox v
45	36	78.3	132	3	AAY92776	Aay92776 Orf virus

ALIGNMENTS

RESULT 1
AAU04525

```
ID   AAU04525 standard; peptide; 8 AA.
XX
AC   AAU04525;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based monocyclic peptide 2.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Disulfide-bond 1..8
FT                  /note= "This bond cyclises the peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Claim 49; Page 32; 102pp; English.
XX
CC   The sequence represents a monomeric monocyclic peptide of the invention,
CC   whose 3-dimensional structure is modeled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
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CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 8 AA;

Query Match       100.0%;   Score 46;  DB 4;  Length 8;
Best Local Similarity      100.0%;   Pred. No. 1.4e+06;
Matches     8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1  CNEESLIC 8
          ||||||||
Db     1  CNEESLIC 8

RESULT 2
AAU04528
ID   AAU04528 standard; protein; 9 AA.
XX
AC   AAU04528;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #2.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key          Location/Qualifiers
FT   Disulfide-bond  1
FT          /note= "A disulfide bond forms between residue 1 and
FT          residue 1 of an identical peptide to form a dimeric
FT          peptide, or between residue 1 and residue 17 of the
FT          sequence appearing as AAU04527 also forming a dimeric
FT          peptide"
FT   Disulfide-bond  2..9
FT          /note= "This bond cyclises the peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
```

```
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cycling a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Claim 59; Page 32; 102pp; English.
XX
CC   The sequence represents a dimeric bicyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 9 AA;

Query Match       100.0%;      Score 46;  DB 4;  Length 9;
Best Local Similarity  100.0%;      Pred. No. 1.4e+06;
Matches     8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1  CNEESLIC 8
          ||||||||
Db     2  CNEESLIC 9

RESULT 3
AAU04522
ID   AAU04522 standard; protein; 73 AA.
XX
AC   AAU04522;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human VEGF-D amino acids Val101-Thr 173.
XX
KW   Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
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PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 1; Page 90-91; 102pp; English.
XX
CC   The sequence represents Human VEGF-D (vascular endothelial growth factor)
CC   amino acids Val101-Thr 173, used together with the C-terminal 23 residues
CC   of VEGF to make a hybrid theoretical molecule for 3 dimensional
CC   modelling. The sequence is used in a method of producing a monomeric
CC   monocyclic peptide by a measuring beta-beta carbon separation distances
CC   on opposite antiparallel strands of a peptide loop fragment from an
CC   exposed loop of a growth factor protein and cyclising the peptide by
CC   oxidising the cysteine residues. The monocyclic peptides, dimeric
CC   bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
CC   peptide with at least one amino acid deleted prior to cyclisation are
CC   used to interfere with angiogenesis, neovascularisation or
CC   lymphangiogenesis in a mammal with a condition characterised by
CC   angiogenesis, neovascularisation or lymphangiogenesis. The condition is
CC   diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
CC   malignant or benign tumour, post-recovery cerebrovascular accident, post-
CC   angioplasty restenosis, head, heat or cold trauma, substance-induced
CC   neovascularisation of the liver, excessive hormone-related angiogenic
CC   dysfunction, diabetes induced neovascular sequelae, hypertension induced
CC   neovascular sequelae, or chronic liver infection. The peptides are also
CC   used to modulate vascular permeability in a mammal (the mammal has a
CC   condition characterised by fluid accumulation in peripheral limbs or in
CC   lungs, peritoneal cavity, pleura, or brain. The peptides are used to
CC   image blood vessels and lymphatic vasculature. The monomeric and bicyclic
CC   peptides are used to interfere with at least one biological activity
CC   induced by VEGF, VEGF-C or -D and are also used in combination with an
CC   anti-inflammatory agent, to treat a chronic inflammation, especially
CC   rheumatoid arthritis, psoriasis and diabetic retinopathy
XX
SQ   Sequence 73 AA;

Query Match   100.0%; Score 46; DB 4; Length 73;
Best Local Similarity   100.0%; Pred. No. 1.1;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
             ||||||||
Db   46 CNEESLIC 53

RESULT 4
AAU04520
ID   AAU04520 standard; protein; 96 AA.
XX
AC   AAU04520;
XX
DT   26-SEP-2001 (first entry)
XX
DE   Human VEGF-D amino acids Val101-PRO186.
XX
KW   Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200152875-A1.
XX

PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 1; Page 89; 102pp; English.
XX
CC   The sequence represents Human VEGF-D (vascular endothelial growth factor)
CC   amino acids Val101-PRO186. The sequence is used in a method of producing
CC   a monomeric monocyclic peptide by a measuring beta-beta carbon separation
CC   distances on opposite antiparallel strands of a peptide loop fragment
CC   from an exposed loop of a growth factor protein and cyclising the peptide
CC   by oxidising the cysteine residues. The monocyclic peptides, dimeric
CC   bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
CC   peptide with at least one amino acid deleted prior to cyclisation are
CC   used to interfere with angiogenesis, neovascularisation or
CC   lymphangiogenesis in a mammal with a condition characterised by
CC   angiogenesis, neovascularisation or lymphangiogenesis. The condition is
CC   diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
CC   malignant or benign tumour, post-recovery cerebrovascular accident, post-
CC   angioplasty restenosis, head, heat or cold trauma, substance-induced
CC   neovascularisation of the liver, excessive hormone-related angiogenic
CC   dysfunction, diabetes induced neovascular sequelae, hypertension induced
CC   neovascular sequelae, or chronic liver infection. The peptides are also
CC   used to modulate vascular permeability in a mammal (the mammal has a
CC   condition characterised by fluid accumulation in peripheral limbs or in
CC   lungs, peritoneal cavity, pleura, or brain. The peptides are used to
CC   image blood vessels and lymphatic vasculature. The monomeric and bicyclic
CC   peptides are used to interfere with at least one biological activity
CC   induced by VEGF, VEGF-C or -D and are also used in combination with an
CC   anti-inflammatory agent, to treat a chronic inflammation, especially
CC   rheumatoid arthritis, psoriasis and diabetic retinopathy
XX
SQ   Sequence 96 AA;

Query Match   100.0%; Score 46; DB 4; Length 96;
Best Local Similarity   100.0%; Pred. No. 1.4;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
             ||||||||
Db   46 CNEESLIC 53

RESULT 5
AAY23889
ID   AAY23889 standard; protein; 109 AA.
XX
AC   AAY23889;
XX
DT   21-SEP-1999 (first entry)
XX
DE   Human vascular endothelial growth factor (VEGF)-D.
XX
KW   vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma;
KW   tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft;
KW   wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.
XX
OS   Homo sapiens.
XX

PN   WO9933485-A1.
XX
PD   08-JUL-1999..
XX
PF   23-DEC-1998;   98WO-US027373.
XX
PR   24-DEC-1997;   97AU-00001131.
PR   29-MAY-1998;   98US-0087392P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Stacker SA, Alitalo K;
XX
DR   WPI; 1999-405368/34.
XX
PT   A human cell line stably expressing vascular endothelial growth factor D,
PT   useful for treating melanomas or tumors expressing VEGF-D.
XX
PS   Claim 6; Page 72; 79pp; English.
XX
CC   The present sequence represents human vascular endothelial growth factor
CC   (VEGF)-D. The specification describes a human cell line which stably
CC   expresses VEGF-D, or fragments/analogues having VEGF-D biological
CC   activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex
CC   DNA, VEGF-D variants or antibodies (especially chimeric antibodies), are
CC   useful for the treatment or alleviation of malignant melanomas, tumours
CC   or psoriasis. Angiogenesis and lymphangiogenesis stimulating amounts of
CC   VEGF-D can be administered to enhance the acceptance and/or healing of
CC   skin grafts or to stimulate the healing of a surgical or traumatic wound
CC   to the skin. Lymphangiogenesis stimulating amounts of VEGF-D can be used
CC   to treat lymphedema. Endothelial proliferation stimulating amounts of
CC   VEGF-D are used to treat scleroderma. Vascularisation stimulating amounts
CC   of VEGF-D can be used to treat anhydrotic ectodermal dysplasia. VEGF-D
CC   antibodies are useful for detecting tumours expressing VEGF-D. Fully-
CC   processed VEGF-D can be used to stimulate at least one VEGF-D bioactivity
CC   chosen from endothelial cell proliferation, migration, survival and
CC   differentiation and lymphangiogenesis without inducing vascular
CC   permeability
XX
SQ   Sequence 109 AAs;

Query Match   100.0%; Score 46; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
          ||||||||
Db   54 CNEESLIC 61

RESULT 6
AAB11931
ID   AAB11931 standard; protein; 109 AA.
XX
AC   AAB11931;
XX
DT   20-NOV-2000 (first entry)
XX
DE   Human truncated VEGF-D.
XX
KW   Truncated VEGF-D; vascular endothelial growth factor; human;
KW   monoclonal antibody; VEGF receptor; VEGFR-2; VEGFR-3;
KW   vascular permeability disorder; endothelial cell proliferative disorder;
KW   angiogenic disorder; lymphangiogenic disorder;
KW   neovascularisation disorder; endothelial cell differentiation disorder;
KW   cancer; diabetic retinopathy; psoriasis; arthropathy; pulmonary oedema;
KW   detection; diagnosis; imaging; lymphatic vasculature.
XX
OS   Homo sapiens.
XX
PN   WO200037025-A2.
XX
PD   29-JUN-2000.

XX
PF   21-DEC-1999;   99WO-US031332.
XX
PR   21-DEC-1998;   98US-0113254P.
PR   17-MAY-1999;   99US-0134556P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Stacker SA;
XX
DR   WPI; 2000-442498/38.
XX
PT   Novel compositions comprising antibodies reactive to vascular endothelial
PT   growth factor-D, useful for treating, e.g. angiogenesis, lymphogiogenesis
PT   and neovascularization disorders.
XX
PS   Claim 1; Fig 1; 44pp; English.
XX
CC   This sequence represents a 109 amino acid truncated human VEGF-D
CC   (vascular endothelial growth factor D), lacking both the N- and C-
CC   terminal regions. The invention relates to a monoclonal antibody, or
CC   fragments thereof, which is specifically reactive with the truncated
CC   human VEGF-D, and methods of preparing the antibody. The antibody of the
CC   invention interferes with the binding of VEGF-D to the VEGF receptors
CC   VEGFR-2 and VEGFR-3, but does not interfere with the binding of VEGF to
CC   these receptors and additionally is not reactive with VEGF-C. The
CC   antibody may be used to treat disorders associated with vascular
CC   permeability, endothelial cell proliferation, angiogenesis,
CC   lymphangiogenesis, neovascularisation and endothelial cell
CC   differentiation, especially cancer, diabetic retinopathy, psoriasis, and
CC   arthropathies. The antibody may also be used to treat fluid accumulation
CC   in the heart and/or lung via modulation of vascular permeability. It may
CC   additionally be used to detect VEGF-D and may be used to image lymphatic
CC   vasculature in tissue
XX
SQ   Sequence 109 AA;

Query Match   100.0%; Score 46; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
          ||||||||
Db   54 CNEESLIC 61

RESULT 7
ABB84621
ID   ABB84621 standard; protein; 109 AA.
XX
AC   ABB84621;
XX
DT   01-APR-2003 (first entry)
XX
DE   Human wild-type VEGF-D monomer SEQ ID 3.
XX
KW   Human; single-chain; extracellular ligand-binding domain; VEGF;
KW   vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
KW   VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
KW   lymphangiogenesis.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Region   8..18
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"
FT   Region   36..49
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"
FT   Region   55..60
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"

FT *Misc-difference* 281
FT   /note= "Encoded by TAA, an in frame stop codon which
FT   interrupts the coding region as shown in Figure 1A-B.
FT   This site is the end of the protein sequence represented
FT   in SEQ ID 1 of the Sequence listing"
FT Region   282..287
FT   /note= "Region not represented in SEQ ID 1 of the
FT   Sequence listing"
XX
PN US200215538-A1.
XX
PD 24-OCT-2002.
XX
PF 09-JAN-2002; 2002US-00044622.
XX
PR 23-JAN-1997; 97US-0078812.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Goli SK, Murry LE;
XX
DR WPI; 2003-182635/18.
DR N-PSDB; ABQ77105.
XX
PT New endothelial growth factor polypeptide and polynucleotides, useful for
PT diagnosing, preventing, and treating cancer and other conditions or
PT diseases involving angiogenesis and cell proliferation.
XX
PS Claim 1; Fig 1A-B; 28pp; English.
XX
CC This invention describes a novel human endothelial growth factor
CC polypeptide which has cytostatic activity. The polypeptide and its
CC encoding polynucleotide are useful in the diagnosis, prevention, and
CC treatment of cancer and other conditions or diseases involving
CC angiogenesis and cell proliferation. NVR may also be used to promote
CC revascularisation following traumatic amputation and surgical
CC reconstruction or added to a tissue culture to promote vasculogenesis in
CC tissues for autologous or heterologous transplant. Antagonists or
CC inhibitors of NVR may be used to suppress or prevent angiogenesis and
CC thus prevent the growth and development of cancers such as cancer of the
CC brain, breast, intestine, kidney, lung, ovary, pancreas, prostate or
CC uterus. The products of the invention can be used for gene therapy. This
CC sequence represents the human NVR protein described in the disclosure of
CC the invention
XX
SQ Sequence 287 AA;

Query Match   100.0%; Score 46; DB 6; Length 287;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches   8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CNEESLIC 8
           ||||||||
Db   146 CNEESLIC 153

RESULT 9
AAW53240
ID AAW53240 standard; protein; 325 AA.
XX
AC AAW53240;
XX
DT 03-AUG-1998 (first entry)
XX
DE Homo sapiens vascular endothelial growth factor D (VEGF-D).
XX
KW vascular endothelial growth factor; VEGF-D; angiogenesis; modification;
KW acceleration; wound healing; tissue; organ; transplants;
KW collateral circulation; infarction; arterial stenosis;
KW coronary artery disease; inhibition; cancer; treatment;
KW diabetic retinopathy; lung disorders; blood circulation;
KW gaseous exchange; chronic obstructive airway disease;
KW intestinal malabsorptive syndrome; biopsy; metastatic risk; detection;

FT *Misc-difference* 60
FT   /note= "This residues is described as Gln in Claim 9"
FT Region   70..86
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"
XX
PN WO200281520-A2.
XX
PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-DK000233.
XX
PR 06-APR-2001; 2001DK-00000578.
PR 06-APR-2001; 2001US-0282239P.
XX
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Boesen TP, Halkier T;
XX
DR WPI; 2003-058505/05.
XX
PT Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds
PT to extracellular ligand-binding domain of vascular endothelial growth
PT factor type 2/type 3 receptor but does not activate the receptor.
XX
PS Claim 9; Page 66; 71pp; English.
XX
CC This invention describes a novel single-chain dimeric polypeptide which
CC binds to extracellular ligand-binding domain of vascular endothelial
CC growth factor (VEGF) type 2 receptor (KDR) or VEGF type 3 receptor (Flt-
CC 4). The polypeptide of the invention comprises two receptor-binding sites
CC of which one is capable of binding to a ligand-binding domain of the
CC receptor and one is incapable of effectively binding to a ligand-binding
CC domain of the receptor, and at least one monomer of the dimeric
CC polypeptide is derived from VEGF, VEGF-C or VEGF-D, where the polypeptide
CC is capable of binding to the receptor, but incapable of activating the
CC receptor. The polypeptide of the invention is useful for preparing a
CC medicament for preventing or treating a disease or condition involving
CC increased signal transduction from, or an increased activation of a VEGF
CC type 2 or type 3 receptor e.g. for inhibiting angiogenesis or
CC lymphangiogenesis. This sequence represents a human single-chain VEGF-D
CC monomer which can be modified and used in the construction of a VEGF-
CC based KDR antagonist described in the disclosure of the invention
XX
SQ Sequence 109 AA;

Query Match   100.0%; Score 46; DB 6; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches   8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CNEESLIC 8
           ||||||||
Db   54 CNEESLIC 61

RESULT 8
ABG73779
ID ABG73779 standard; protein; 287 AA.
XX
AC ABG73779;
XX
DT 03-APR-2003 (first entry)
XX
DE Human NVR protein.
XX
KW NVR; human; endothelial growth factor; cytostatic; cancer; angiogenesis;
KW cell proliferation; revascularisation; amputation; vasculogenesis;
KW prostate; uterus; gene therapy.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers

```
KW   diagnosis; congestive heart failure.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   Region         126..128
FT                  /note= "potential N-linked glycosylation site"
FT   Region         156..158
FT                  /note= "potential N-linked glycosylation site"
FT   Region         258..260
FT                  /note= "potential N-linked glycosylation site"
XX
PN   WO9807832-A1.
XX
PD   26-FEB-1998.
XX
PF   21-AUG-1997;    97WO-US014696.
XX
PR   23-AUG-1996;    96AU-00001825.
PR   23-AUG-1996;    96US-0023751P.
PR   11-NOV-1996;    96AU-00003554.
PR   14-NOV-1996;    96US-0031097P.
PR   05-FEB-1997;    97AU-00004954.
PR   10-FEB-1997;    97US-0038814P.
PR   19-JUN-1997;    97AU-0007435.
PR   01-JUL-1997;    97US-0051426P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
PI   Achen MG,  Wilks AF,  Stacker SA,  Alitalo K;
XX
DR   WPI; 1998-179057/16.
DR   N-PSDB; AAV20806.
XX
PT   New isolated vascular endothelial growth factor-D - used to develop
PT   products for use in e.g. modifying angiogenesis or treating lung, heart
PT   or intestinal disorders.
XX
PS   Claim 16; Page 57-58; 101pp; English.
XX
CC   The sequence is that of human breast vascular endothelial growth factor D
CC   (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in
CC   wound healing, tissue or organ transplantation, or to establish
CC   collateral circulation in tissue infarction or arterial stenosis, such as
CC   coronary artery disease, and inhibition of angiogenesis in the treatment
CC   of cancer or of diabetic retinopathy. It can also be used in the
CC   treatment of lung disorders to improve blood circulation in the lung
CC   and/or gaseous exchange between the lungs and the blood stream or to
CC   improve blood circulation to the heart and O2 gas permeability in cases
CC   of cardiac insufficiency, to improve blood flow and gaseous exchange in
CC   chronic obstructive airway disease, or to treat malabsorptive syndromes
CC   in the intestinal tract. Quantitation of VEGF-D in cancer biopsy
CC   specimens may be useful as an indicator of future metastatic risk.
CC   Antagonists can be used for treating e.g. conditions such as congestive
CC   heart failure, involving accumulations of fluid in the lung resulting
CC   from increases in vascular permeability. The products can also be used
CC   for detection and diagnosis
XX
SQ   Sequence 325 AA;

Query Match             100.0%;  Score 46;  DB 2;  Length 325;
Best Local Similarity   100.0%;  Pred. No. 4.6;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CNEESLIC 8
              ||||||||
Db        117 CNEESLIC 124
```

```
XX
AC   AAY97572;
XX
DT   05-APR-2001  (first entry)
XX
DE   Human VEGF-D protein sequence.
XX
KW   Human; angiogenic protein; wound healing; vascular tissue repair;
KW   peripheral arterial disease; critical limb ischaemia; coronary disease;
KW   angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis;
KW   rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
KW   infectious disease; neurodegeneration;
KW   vascular endothelial growth factor-D; VEGF-D.
XX
OS   Homo sapiens.
XX
PN   WO200075163-A1.
XX
PD   14-DEC-2000.
XX
PF   01-JUN-2000; 2000WO-US014925.
XX
PR   03-JUN-1999;   99US-0137796P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM,  Hu J,  Cao L;
XX
DR   WPI; 2001-071057/08.
DR   N-PSDB; AAA91006.
XX
PT   New nucleic acid encoding angiogenic proteins, useful e.g. for promoting
PT   healing of wounds and treating peripheral arterial disease, critical limb
PT   ischemia or coronary disease.
XX
PS   Claim 11; Page 226-227; 244pp; English.
XX
CC   This sequence is vascular endothelial growth factor-D (VEGF-D), which is
CC   an angiogenic protein of the invention. The angiogenic proteins and the
CC   DNA sequences encoding them, are used to prevent, treat or ameliorate
CC   disease and to detect diseases, or susceptibility, by detecting mutations
CC   or the presence or amount of angiogenic protein expression. Particularly
CC   they are used to stimulate wound healing, growth of damaged bone and
CC   tissue, and for repair of vascular tissue, especially peripheral arterial
CC   disease, critical limb ischaemia or coronary disease. Antagonists of the
CC   sequences are used to inhibit angiogenesis in tumours and to treat
CC   inflammation (where associated with increased vascular permeability),
CC   diabetic retinopathy, rheumatoid arthritis or psoriasis. Agonists are
CC   also useful for stimulating (lymph)angiogenesis. The proteins are also
CC   used to identify specific binding agents (potential therapeutic agents)
CC   and to raise antibodies. The antibodies are useful as therapeutic
CC   (ant)agonists; for detection, purification and targeting of proteins for
CC   in vivo or in vitro diagnosis (including imaging) or for therapy
CC   (including when linked to e.g. a label or cytotoxin), and for
CC   immunotyping of cells, e.g. for detecting minimal residual disease or
CC   haematopoietic progenitor/stem cells. It is also contemplated that the
CC   sequences might be useful for treating a very wide range of other
CC   disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases
CC   (viral, bacterial, fungal or parasitic); neurodegeneration, also as
CC   chemotactic agents or for stimulating regeneration of the nervous system
CC   etc
XX
SQ   Sequence 325 AA;

Query Match             100.0%;  Score 46;  DB 4;  Length 325;
Best Local Similarity   100.0%;  Pred. No. 4.6;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CNEESLIC 8
              ||||||||
Db        117 CNEESLIC 124
```

```
RESULT 10
AAY97572
ID   AAY97572 standard; protein; 325 AA.
```

```
RESULT 11
AAW44293
ID   AAW44293 standard; protein; 354 AA.
XX
AC   AAW44293;
XX
DT   22-JUN-1998  (first entry)
XX
DE   Human vascular endothelial growth factor D.
XX
KW   Human; vascular endothelial growth factor D; VEGF-D; gene therapy;
KW   inflammation; oedema.
XX
OS   Homo sapiens.
XX
PN   WO9802543-A1.
XX
PD   22-JAN-1998.
XX
PF   15-JUL-1997;  97WO-JP002456.
XX
PR   15-JUL-1996;  96JP-00185216.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Hirata Y, Nezu J;
XX
DR   WPI; 1998-110591/10.
DR   N-PSDB; AAV15156.
XX
PT   VEGF-D protein encoded by DNA - useful for, e.g. gene therapy and
PT   treating oedema.
XX
CC   The present sequence represents human vascular endothelial growth factor
CC   D (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind
CC   the protein, may be useful in, e.g. gene therapy and in treatment of
CC   inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D
CC   DNA sequences may be used for screening for the compounds which bind to
CC   the VEGF-D protein
XX
SQ   Sequence 354 AA;

Query Match             100.0%;  Score 46;  DB 2;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 5;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CNEESLIC 8
              ||||||||
Db        146 CNEESLIC 153

RESULT 12
AAW49036
ID   AAW49036 standard; protein; 354 AA.
XX
AC   AAW49036;
XX
DT   26-OCT-1998  (first entry)
XX
DE   Human zvegf2 growth factor.
XX
KW   Human zvegf2 growth factor; mitogen; fibroblast; smooth muscle cell;
KW   venous stasis ulcer; diabetic ulcer; skin wound; chemotactic effect;
KW   angiogenic effect; tumour; diabetic retinopathy; psoriasis; arthritis;
KW   scleroderma.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..23
FT                   /note= "Signal peptide"
FT   Peptide         24..108
FT                   /note= "Pro-region"
FT   Binding-site    109..197
FT                   /note= "Receptor binding domain"
FT   Region          206..256
FT                   /note= "Cysteine-rich domain"
FT   Region          257..274
FT                   /note= "Balbiani ring motif"
FT   Region          275..294
FT                   /note= "Balbiani ring motif"
FT   Region          295..354
FT                   /note= "Cysteine-rich domain""
XX
PN   WO9824811-A2.
XX
PD   11-JUN-1998.
XX
PF   20-NOV-1997;  97WO-US020888.
XX
PR   06-DEC-1996;  96US-00759657.
PR   18-SEP-1997;  97US-0093455.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Gilbert T, Conklin DC, Hart CE, Nygaard S, Sheppard PO;
XX
DR   WPI; 1998-333256/29.
DR   N-PSDB; AAV32823.
XX
PT   New isolated vascular endothelial growth factor - used to develop
PT   products for treating e.g. wounds, burns, myocardial infarction, tumours,
PT   psoriasis, arthritis, restenosis or organ transplants,
XX
PS   Claim 1; Page 53-54; 77pp; English.
XX
CC   The present sequence represents a human zvegf2 growth factor encoded by
CC   the zvegf2 cDNA which was isolated from a human heart cDNA library.
CC   zvegf2 protein in a dimeric form acts as a mitogen for fibroblasts or
CC   smooth muscle cells. zvegf2 is claimed to be useful for stimulating the
CC   revascularisation of tissue or the re-endothelialisation of vascular
CC   tissue. zvefg2 is particularly claimed to be useful for the treatment of
CC   full-thickness skin wounds, including venous stasis ulcers and diabetic
CC   ulcers. The zvegf2 protein is also claimed to be useful as an additive in
CC   tissue adhesives for promoting revascularisation of the healing tissue.
CC   Antagonists against zvegf2 can be used to block its mitogenic,
CC   chemotactic and angiogenic effects. The antagonists may therefore be
CC   useful for reducing growth of solid tumours by inhibiting
CC   neovascularisation of the developing tumour or by directly blocking
CC   tumour cell growth, in the treatment of diabetic retinopathy, psoriasis,
CC   arthritis, and scleroderma
XX
SQ   Sequence 354 AA;

Query Match             100.0%;  Score 46;  DB 2;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 5;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CNEESLIC 8
              ||||||||
Db        146 CNEESLIC 153

RESULT 13
AAW53241
ID   AAW53241 standard; protein; 354 AA.
XX
AC   AAW53241;
XX
DT   03-AUG-1998  (first entry)
XX
DE   Homo sapiens vascular endothelial growth factor D (VEGF-D).
XX
KW   vascular endothelial growth factor; VEGF-D; angiogenesis; modification;
```

KW   acceleration; wound healing; tissue; organ; transplants;
KW   collateral circulation; infarction; arterial stenosis;
KW   coronary artery disease; inhibition; cancer; treatment;
KW   diabetic retinopathy; lung disorders; blood circulation;
KW   gaseous exchange; chronic obstructive airway disease;
KW   intestinal malabsorptive syndrome; biopsy; metastatic risk; detection;
KW   diagnosis; congestive heart failure.
XX
OS   Homo sapiens.
XX
PN   WO9807832-A1.
XX
PD   26-FEB-1998.
XX
PF   21-AUG-1997;   97WO-US014696.
XX
PR   23-AUG-1996;   96AU-00001825.
PR   23-AUG-1996;   96US-0023751P.
PR   11-NOV-1996;   96AU-00003554.
PR   14-NOV-1996;   96US-0031097P.
PR   05-FEB-1997;   97AU-00004954.
PR   10-FEB-1997;   97US-0038814P.
PR   19-JUN-1997;   97AU-00007435.
PR   01-JUL-1997;   97US-0051426P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
PI   Achen MG, Wilks AF, Stacker SA, Alitalo K;
XX
DR   WPI; 1998-179057/16.
DR   N-PSDB; AAV20807.
XX
PT   New isolated vascular endothelial growth factor-D - used to develop
PT   products for use in e.g. modifying angiogenesis or treating lung, heart
PT   or intestinal disorders.
XX
PS   Claim 16; Page 60-61; 101pp; English.
XX
CC   The sequence is that of human lung vascular endothelial growth factor D
CC   (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in
CC   wound healing, tissue or organ transplantation, or to establish
CC   collateral circulation in tissue infarction or arterial stenosis, such as
CC   coronary artery disease, and inhibition of angiogenesis in the treatment
CC   of cancer or of diabetic retinopathy. It can also be used in the
CC   treatment of lung disorders to improve blood circulation in the lung
CC   and/or gaseous exchange between the lungs and the blood stream or to
CC   improve blood circulation to the heart and O2 gas permeability in cases
CC   of cardiac insufficiency, to improve blood flow and gaseous exchange in
CC   chronic obstructive airway disease, or to treat malabsorptive syndromes
CC   in the intestinal tract. Quantitation of VEGF-D in cancer biopsy
CC   specimens may be useful as an indicator of future metastatic risk.
CC   Antagonists can be used for treating e.g. conditions such as congestive
CC   heart failure, involving accumulations of fluid in the lung resulting
CC   from increases in vascular permeability. The products can also be used
CC   for detection and diagnosis
XX
SQ   Sequence 354 AA;

Query Match   100.0%; Score 46; DB 2; Length 354;
Best Local Similarity   100.0%; Pred. No. 5;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
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Db   146 CNEESLIC 153

RESULT 14
AAB10649
ID   AAB10649 standard; protein; 354 AA.
XX
AC   AAB10649;

XX
DT   19-JAN-2001 (first entry)
XX
DE   Human VEGD protein.
XX
KW   VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;
KW   antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW   angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW   rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW   tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW   venous sore; diabetic ulcer; burns; skin graft growth; VEGD.
XX
OS   Homo sapiens.
XX
PN   WO200037641-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US030503.
XX
PR   22-DEC-1998;   98GB-00028377.
PR   18-MAR-1999;   99US-0124967P.
PR   08-NOV-1999;   99US-0164131P.
XX
PA   (JANC) JANSSEN PHARM NV.
XX
PI   Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI   Dhanaraj SN, Xu J;
XX
DR   WPI; 2000-442669/38.
XX
PT   New vascular endothelial growth factor protein, useful for treating or
PT   preventing diseases associated with inappropriate angiogenesis activity
PT   such as cancer, rheumatoid arthritis, psoriasis and wounds.
XX
PS   Disclosure; Fig 11; 127pp; English.
XX
CC   This invention describes a novel vascular endothelial growth factor-X
CC   (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC   vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC   antidiabetic activity and acts as an angiogenesis and vascularization
CC   regulator. An antisense molecule of the invention is useful for treating
CC   or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC   retinopathy by inhibiting angiogenic activity or inappropriate
CC   vascularization including formation and proliferation of new blood
CC   vessels, growth and development of tissues, tissue regeneration and organ
CC   and tissue repair in a subject. The products of the invention are useful
CC   for preparing medicaments for treating wounds such as dermal ulcers,
CC   pressure sores, venous sores, diabetic ulcers and burns and to promote
CC   skin graft growth, tissue repair, proliferation of new blood vessels,
CC   tissue regeneration and organ repair by promoting angiogenic activity or
CC   vascularization. This sequence represents the human VEGD protein used to
CC   illustrate the method of the invention
XX
SQ   Sequence 354 AA;

Query Match   100.0%; Score 46; DB 3; Length 354;
Best Local Similarity   100.0%; Pred. No. 5;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
              ||||||||
Db   146 CNEESLIC 153

RESULT 15
AAY70750
ID   AAY70750 standard; protein; 354 AA.
XX
AC   AAY70750;
XX
DT   17-AUG-2000 (first entry)
XX

DE Human prepro-vascular endothelial growth factor D.

XX

KW Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4;
KW VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35;
KW cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis;
KW neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;
KW sarcoma; malignancy; VEGF-D; vascular endothelial growth factor D.

XX

OS Homo sapiens.

XX

PN WO20021560-A1.

XX

PD 20-APR-2000.

XX

PF 08-OCT-1999; 99WO-US023525.

XX

PR 09-OCT-1998; 98US-00169079.

XX

PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX

PI Alitalo K, Kaipainen A, Valltola R, Jussila L;

XX

DR WPI; 2000-317850/27.

XX

PT Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and
PT sarcomas, involves administering a compound capable of inhibiting binding
PT of ligand proteins to fms-like tyrosine kinase-1 receptor.

XX

PS Example 15-17; Page 142-143; 148pp; English.

XX

CC The patent discloses a method to treat neoplastic disease characterised
CC by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also
CC referred as vascular endothelial growth factor receptor-3, VEGFR-3) in
CC endothelial cells of blood vessels adjacent to malignant neoplasm. The
CC method involves administering a compound that inhibits binding of a
CC ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular
CC endothelial cells. The compound is useful for treating neoplastic disease
CC such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas
CC and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used
CC for manufacturing medicament useful for diagnostic screening, imaging and
CC treatment of malignancies characterised by Flt4-expressing blood cells.
CC The Flt4 gene maps to chromosomal region 5q35 and is expressed as 5.8 kb
CC and 4.5 kb mRNAs which differ in their 3' sequences and are
CC differentially expressed in HEL and DAMI cell lines. Flt4 belongs to a
CC subfamily of class III receptor tyrosine kinases (RTKs). It is used as a
CC target for tumour imaging and anti-tumour therapy. The present sequence
CC is a human prepro-vascular endothelial growth factor D (VEGF-D), a
CC specific example of Flt4 binding compound. A recombinantly matured VEGF-D
CC lacking residues 1-92 and 202-354 retains the ability to activate VEGFR-2
CC and VEGFR-3 receptors and associate as non-covalently linked dimers

XX

SQ Sequence 354 AA;

Query Match   100.0%; Score 46; DB 3; Length 354;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
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Db 146 CNEESLIC 153

Search completed: September 5, 2004, 09:55:10
Job time : 27.2626 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:00:15 ; Search time 22.4646 Seconds
(without alignments)
112.199 Million cell updates/sec

Title: US-09-761-636A-6
Perfect score: 46
Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1298764 segs, 315065143 residues

Total number of hits satisfying chosen parameters: 1298764

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	100.0	8	9	US-09-761-636A-6	Sequence 6, Appli
2	46	100.0	9	9	US-09-761-636A-9	Sequence 9, Appli
3	46	100.0	73	9	US-09-761-636A-3	Sequence 3, Appli
4	46	100.0	96	9	US-09-761-636A-1	Sequence 1, Appli
5	46	100.0	109	9	US-09-956-095-3	Sequence 3, Appli
6	46	100.0	109	9	US-09-219-345A-1	Sequence 1, Appli
7	46	100.0	109	16	US-10-779-731-1	Sequence 1, Appli
8	46	100.0	197	12	US-10-352-153-8	Sequence 1, Appli
9	46	100.0	280	13	US-10-044-622-1	Sequence 1, Appli
10	46	100.0	325	14	US-10-274-953-3	Sequence 3, Appli
11	46	100.0	325	14	US-10-161-694-3	Sequence 3, Appli
12	46	100.0	354	9	US-09-956-095-2	Sequence 2, Appli
13	46	100.0	354	9	US-09-219-345A-11	Sequence 11, Appl
14	46	100.0	354	9	US-09-795-006A-119	Sequence 119, App
15	46	100.0	354	10	US-09-375-248-6	Sequence 6, Appli
16	46	100.0	354	12	US-09-765-534B-22	Sequence 22, Appl
17	46	100.0	354	12	US-10-661-740-6	Sequence 6, Appli
18	46	100.0	354	14	US-10-262-538-26	Sequence 26, Appli
19	46	100.0	354	14	US-10-274-953-5	Sequence 5, Appli
20	46	100.0	354	14	US-10-161-694-5	Sequence 5, Appli
21	43	93.5	8	9	US-09-761-636A-20	Sequence 20, Appl
22	42	91.3	8	9	US-09-761-636A-22	Sequence 22, Appl
23	41	89.1	8	9	US-09-761-636A-19	Sequence 19, Appl
24	41	89.1	9	9	US-09-761-636A-33	Sequence 33, Appl
25	40	87.0	9	9	US-09-761-636A-34	Sequence 34, Appl
26	39	84.8	8	9	US-09-761-636A-21	Sequence 21, Appl
27	39	84.8	354	14	US-10-174-930-1	Sequence 1, Appli
28	39	84.8	362	13	US-10-139-876-4	Sequence 4, Appli
29	37	80.4	172	12	US-10-424-599-211285	Sequence 211285,
30	36	78.3	49	13	US-10-139-876-11	Sequence 11, Appl
31	36	78.3	81	13	US-10-086-623-18	Sequence 18, Appl
32	36	78.3	81	14	US-10-260-539-18	Sequence 18, Appl
33	36	78.3	110	10	US-09-847-524-6	Sequence 6, Appli
34	36	78.3	132	9	US-09-795-006A-151	Sequence 151, App
35	36	78.3	132	12	US-10-352-153-11	Sequence 11, Appl
36	36	78.3	133	9	US-09-852-209A-11	Sequence 11, Appl
37	36	78.3	133	12	US-10-439-337A-11	Sequence 11, Appl
38	36	78.3	133	12	US-10-303-997B-11	Sequence 4, Appli
39	36	78.3	133	14	US-10-352-153-2	Sequence 2, Appli
40	36	78.3	133	14	US-10-131-600-11	Sequence 11, Appl
41	36	78.3	190	14	US-10-177-485-4	Sequence 4, Appli
42	36	78.3	190	14	US-10-155-492-4	Sequence 4, Appli
43	36	78.3	321	10	US-09-847-524-4	Sequence 4, Appli
44	36	78.3	321	14	US-10-274-953-9	Sequence 9, Appli
45	36	78.3	321	14	US-10-161-694-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-761-636A-6
; Sequence 6, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-6

Query Match   100.0%;   Score 46; DB 9; Length 8;
Best Local Similarity 100.0%;   Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CNEESLIC 8
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Db   1 CNEESLIC 8

RESULT 2
US-09-761-636A-9
; Sequence 9, Application US/09761636A
; Patent No. US20020065218A1

GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-9

Query Match   100.0%; Score 46; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches   8; Conservative   0; Mismatches   0; Indels 0; Gaps 0;

Qy   1 CNEESLIC 8
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Db   2 CNEESLIC 9

RESULT 3
US-09-761-636A-3
; Sequence 3, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: 2001-01-18
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid residues Val101-Thr173 of VEGF-D
US-09-761-636A-3

Query Match   100.0%; Score 46; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches   8; Conservative   0; Mismatches   0; Indels 0; Gaps 0;

Qy   1 CNEESLIC 8
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Db   46 CNEESLIC 53

RESULT 4
US-09-761-636A-1
; Sequence 1, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc

; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid residues of Val101-Pro196 of VEGF-D
US-09-761-636A-1

Query Match   100.0%; Score 46; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.88;
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Qy   1 CNEESLIC 8
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Db   46 CNEESLIC 53

RESULT 5
US-09-956-095-3
; Sequence 3, Application US/09956095
; Patent No. US20020102260A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steven A.
; TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
; TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
; TITLE OF INVENTION: VASCULARIZATION OF TISSUE
; FILE REFERENCE: 1064/48666PC
; CURRENT APPLICATION NUMBER: US/09/956,095
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 09/796,714
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/234,196
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-095-3

Query Match   100.0%; Score 46; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 1;
Matches   8; Conservative   0; Mismatches   0; Indels 0; Gaps 0;

Qy   1 CNEESLIC 8
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Db   54 CNEESLIC 61

RESULT 6
US-09-219-345A-1
; Sequence 1, Application US/09219345A
; Patent No. US20020127222A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; TITLE OF INVENTION: EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR

; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING
; TITLE OF INVENTION: MELANOMAS
; FILE REFERENCE: 1064/44385 Marc ACHEN
; CURRENT APPLICATION NUMBER: US/09/219,345A
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: AU PP 1131
; PRIOR FILING DATE: 1997-12-24
; PRIOR APPLICATION NUMBER: US 60/087,392
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-219-345A-1

Query Match   100.0%;   Score 46; DB 9; Length 109;
Best Local Similarity   100.0%;   Pred. No. 1;
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Qy   1 CNEESLIC   8
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Db   54 CNEESLIC 61

RESULT 7
US-10-779-731-1
; Sequence 1, Application US/10779731
; Publication No. US2004141917A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/10/779,731
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US/10/100,037
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/469,186
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113,254
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/134,556
; PRIOR FILING DATE: 1999-05-17
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US-10-779-731-1

Query Match   100.0%;   Score 46; DB 16; Length 109;
Best Local Similarity   100.0%;   Pred. No. 1;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CNEESLIC   8
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Db   54 CNEESLIC 61

RESULT 8
US-10-352-153-8
; Sequence 8, Application US/10352153
; Publication No. US2003021101A1
; GENERAL INFORMATION:
; APPLICANT: Wise, Lyn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stacker, Stephen
; TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF

; TITLE OF INVENTION: VIRUS N22 BINDS AND ACTIVATES MAMMALIAN VEGF
; TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence Listing for 09/431,833
; CURRENT APPLICATION NUMBER: US/10/352,153
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US/09/431,888A
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,689
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,800
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-352-153-8

Query Match   100.0%;   Score 46; DB 12; Length 197;
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Qy   1 CNEESLIC   8
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Db   70 CNEESLIC 77

RESULT 9
US-10-044-622-1
; Sequence 1, Application US/10044622
; Publication No. US2002015538A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
;   Goli, Surya K.
;   Murry, Lynn E.
; TITLE OF INVENTION: NOVEL ENDOTHELIAL GROWTH
;   FACTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/044,622
;   FILING DATE: 09-Jan-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/788,812
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REFERENCE/DOCKET NUMBER: PF-0185 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 280 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: LUNGAST01

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;           CLONE: 873352
;           SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-622-1

Query Match          100.0%;  Score 46;  DB 13;  Length 280;
Best Local Similarity 100.0%;  Pred. No. 2.6;
Matches    8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       1  CNEESLIC  8
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Db     146  CNEESLIC  153

RESULT 10
US-10-274-953-3
; Sequence 3, Application US/10274953
; Publication No. US2003011465BA1
; GENERAL INFORMATION:
;   APPLICANT: Marc G. ACHEN
;   APPLICANT: Andrew F. WILKS
;   APPLICANT: Steven A. STACKER
;   APPLICANT: Kari ALITALO
;   TITLE OF INVENTION: GROWTH FACTOR
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;     STREET: 1200 G Street, NW, Suite 700
;     CITY: Washington
;     STATE: DC
;     COUNTRY: United States of America
;     ZIP: 20005
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/274,953
;     FILING DATE: 22-oct-2002
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/296,275
;     FILING DATE:
;     APPLICATION NUMBER: 08/915,795
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: EVANS, Joseph D.
;     REGISTRATION NUMBER: 26,269
;     REFERENCE/DOCKET NUMBER: 1064/42983
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202) 628-8800
;     TELEFAX: (202) 628-8844
;     TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 325 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ORIGINAL SOURCE:
;     TISSUE TYPE: Human Breast
US-10-274-953-3

Query Match          100.0%;  Score 46;  DB 14;  Length 325;
Best Local Similarity 100.0%;  Pred. No. 3;
Matches    8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       1  CNEESLIC  8
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Db     117  CNEESLIC  124

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; Sequence 3, Application US/10161694
; Publication No. US20030125537A1
; GENERAL INFORMATION:
;   APPLICANT: Marc G. ACHEN
;   APPLICANT: Andrew F. WILKS
;   APPLICANT: Steven A. STACKER
;   APPLICANT: Kari ALITALO
;   TITLE OF INVENTION: GROWTH FACTOR
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;     STREET: 1200 G Street, NW, Suite 700
;     CITY: Washington
;     STATE: DC
;     COUNTRY: United States of America
;     ZIP: 20005
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/161,694
;     FILING DATE: 05-Jun-2002
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/296,275
;     FILING DATE: <Unknown>
;     APPLICATION NUMBER: 08/915,795
;     FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: EVANS, Joseph D.
;     REGISTRATION NUMBER: 26,269
;     REFERENCE/DOCKET NUMBER: 1064/42983
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202) 628-8800
;     TELEFAX: (202) 628-8844
;     TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 325 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ORIGINAL SOURCE:
;     TISSUE TYPE: Human Breast
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-161-694-3

Query Match          100.0%;  Score 46;  DB 14;  Length 325;
Best Local Similarity 100.0%;  Pred. No. 3;
Matches    8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       1  CNEESLIC  8
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Db     117  CNEESLIC  124

RESULT 12
US-09-956-095-2
; Sequence 2, Application US/09956095
; Patent No. US20020102260A1
; GENERAL INFORMATION:
;   APPLICANT: ACHEN, Marc G.
;   APPLICANT: STACKER, Steven A.
;   TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
;   TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
;   TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
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;    TITLE OF INVENTION: VASCULARIZATION OF TISSUE
;    FILE REFERENCE: 1064/48666PC
;    CURRENT APPLICATION NUMBER: US/09/956,095
;    CURRENT FILING DATE: 2001-09-20
;    PRIOR APPLICATION NUMBER: 09/796,714
;    PRIOR FILING DATE: 2001-03-02
;    PRIOR APPLICATION NUMBER: 60/234,196
;    PRIOR FILING DATE: 2000-09-20
;    NUMBER OF SEQ ID NOS: 4
;    SOFTWARE: PatentIn version 3.1
;    SEQ ID NO 2
;    LENGTH: 354
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-956-095-2

Query Match         100.0%;  Score 46;  DB 9;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 3.3;
Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1  CNEESLIC   8
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Db   146  CNEESLIC   153


RESULT 13
US-09-219-345A-11
; Sequence 11, Application US/09219345A
; Patent No. US2002012722A1
; GENERAL INFORMATION:
;    APPLICANT: ACHEN, Marc
;    APPLICANT: ACHEN, Marc
;    TITLE OF INVENTION: EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR
;    TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING
;    TITLE OF INVENTION: MELANOMAS
;    FILE REFERENCE: 1064/44385 Marc ACHEN
;    CURRENT APPLICATION NUMBER: US/09/219,345A
;    CURRENT FILING DATE: 1998-12-23
;    PRIOR APPLICATION NUMBER: AU PP 1131
;    PRIOR FILING DATE: 1997-12-24
;    PRIOR APPLICATION NUMBER: US 60/087,392
;    PRIOR FILING DATE: 1998-05-29
;    NUMBER OF SEQ ID NOS: 11
;    SOFTWARE: PatentIn Ver. 2.0
;    SEQ ID NO 11
;    LENGTH: 354
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-219-345A-11

Query Match         100.0%;  Score 46;  DB 9;  Length 354;
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Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1  CNEESLIC   8
          ||||||||
Db   146  CNEESLIC   153


RESULT 14
US-09-795-006A-119
; Sequence 119, Application US/09795006A
; GENERAL INFORMATION:
;    APPLICANT: Alitalo et al
;    TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
;    TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
;    FILE REFERENCE: 28967/35977B
;    CURRENT APPLICATION NUMBER: US/09/795,006A
;    CURRENT FILING DATE: 2001-02-26
;    PRIOR APPLICATION NUMBER: US 60/205,331
;    PRIOR FILING DATE: 2000-05-18
;    PRIOR APPLICATION NUMBER: US 60/185,205
;    PRIOR FILING DATE: 2000-02-25
;    NUMBER OF SEQ ID NOS: 175
;    SOFTWARE: PatentIn Ver. 2.0
;    SEQ ID NO 119
;    LENGTH: 354
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-795-006A-119

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Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1  CNEESLIC   8
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Db   146  CNEESLIC   153


RESULT 15
US-09-375-248-6
; Sequence 6, Application US/09375248
; Publication No. US2003002675 9A1
; GENERAL INFORMATION:
;    APPLICANT: Ferrell, Robert E.
;    APPLICANT: Alitalo, Kari
;    APPLICANT: Finegold, David N.
;    APPLICANT: Karkkainen, Marika
;    TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
;    TITLE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)
;    FILE REFERENCE: 28967/35255A
;    CURRENT APPLICATION NUMBER: US/09/375,248
;    CURRENT FILING DATE: 1999-08-16
;    EARLIER APPLICATION NUMBER: PCT/US99/06133
;    EARLIER FILING DATE: 1999-03-26
;    NUMBER OF SEQ ID NOS: 28
;    SOFTWARE: PatentIn Ver. 2.0
;    SEQ ID NO 6
;    LENGTH: 354
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-375-248-6

Query Match         100.0%;  Score 46;  DB 10;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 3.3;
Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1  CNEESLIC   8
          ||||||||
Db   146  CNEESLIC   153


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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:55:30 ; Search time 7.11111 Seconds
                                         (without alignments)
                                         58.079 Million cell updates/sec

Title: US-09-761-636A-6
Perfect score: 46
Sequence: 1 CNEESLIC 8
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents AA:*
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             3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
             4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
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2	46	100.0	109	4	US-09-469-185-1	Sequence 1, Appli
3	46	100.0	197	4	US-09-431-888-8	Sequence 8, Appli
4	46	100.0	325	3	US-08-915-795-3	Sequence 3, Appli
5	46	100.0	354	3	US-08-915-795-5	Sequence 5, Appli
6	36	78.3	120	6	5194596-9	Patent No. 5194596
7	36	78.3	120	6	5219739-9	Patent No. 5219739
8	36	78.3	132	4	US-09-125-642C-15	Sequence 15, Appl
9	36	78.3	132	4	US-09-431-888-11	Sequence 11, Appl
10	36	78.3	133	4	US-09-431-888-2	Sequence 2, Appli
11	36	78.3	164	6	5194596-17	Patent No. 5194596
12	36	78.3	164	6	5219739-17	Patent No. 5219739
13	36	78.3	164	6	5219739-18	Patent No. 5219739
14	36	78.3	190	6	5332671-3	Patent No. 5332671
15	36	78.3	321	3	US-08-915-795-9	Sequence 9, Appli
16	36	78.3	358	3	US-08-915-795-8	Sequence 8, Appli
17	33	71.7	146	3	US-08-586-039B-33	Sequence 33, Appl
18	33	71.7	146	4	US-09-699-769-33	Sequence 33, Appl
19	33	71.7	189	1	US-08-469-427A-15	Sequence 15, Appl
20	33	71.7	190	2	US-08-569-063C-20	Sequence 20, Appl
21	33	71.7	190	3	US-08-586-039B-31	Sequence 31, Appl
22	33	71.7	190	4	US-09-699-769-31	Sequence 31, Appl
23	33	71.7	214	3	US-08-586-039B-35	Sequence 35, Appl
24	33	71.7	214	4	US-09-699-769-35	Sequence 35, Appl
25	33	71.7	278	2	US-08-460-309-13	Sequence 13, Appl
26	33	71.7	278	2	US-08-125-077-13	Sequence 13, Appl
27	33	71.7	279	1	US-08-152-019A-29	Sequence 29, Appl
28	33	71.7	1196	1	US-08-144-121-4	Sequence 4, Appli
29	33	71.7	1196	2	US-08-735-893-4	Sequence 4, Appli
30	33	71.7	1765	4	US-09-562-702A-16	Sequence 16, Appl
31	33	71.7	1765	4	US-09-561-818A-16	Sequence 16, Appl
32	33	71.7	1786	4	US-09-562-702A-14	Sequence 14, Appl
33	33	71.7	1786	4	US-09-561-818A-14	Sequence 14, Appl
34	33	71.7	1786	4	US-09-561-709B-9	Sequence 9, Appli
35	32	69.6	12	3	US-08-742-243-43	Sequence 43, Appl
36	32	69.6	12	3	US-08-742-243-44	Sequence 44, Appl
37	32	69.6	12	3	US-08-742-243-45	Sequence 45, Appl
38	32	69.6	65	4	US-09-244-583-12	Sequence 12, Appl
39	32	69.6	109	3	US-08-691-794-3	Sequence 3, Appli
40	32	69.6	110	4	US-09-392-932-11	Sequence 11, Appl
41	32	69.6	110	4	US-09-574-708A-11	Sequence 11, Appl
42	32	69.6	110	4	US-09-822-270-17	Sequence 17, Appl
43	32	69.6	110	4	US-09-392-931-10	Sequence 10, Appl
44	32	69.6	110	4	US-09-392-931-11	Sequence 11, Appl
45	32	69.6	121	6	5194596-19	Patent No. 5194596

ALIGNMENTS

RESULT 1
US-09-469-186-1
; Sequence 1, Application US/09469186
; Patent No. 6383484
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,186
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-186-1

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Best Local Similarity   100.0%; Pred. No. 0.33;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
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Db   54 CNEESLIC 61

RESULT 2
US-09-469-185-1
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; Patent No. 6531185
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,185
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

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; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-185-1

Query Match        100.0%;  Score 46;  DB 4;  Length 109;
Best Local Similarity 100.0%;  Pred. No. 0.33;
Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1  CNEESLIC  8
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Db         54  CNEESLIC  61

RESULT 3
US-09-431-888-8
; Sequence 8, Application US/09431888A
; Patent No. 6541008
; GENERAL INFORMATION:
; APPLICANT: Wise, Lyn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stacker, Stephen
; TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
; TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
; TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence listing for 09/431,833
; Patent No. 6541008
; CURRENT APPLICATION NUMBER: US/09/431,888A
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/106,689
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/106,800
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-888-8

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Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1  CNEESLIC  8
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Db         70  CNEESLIC  77

RESULT 4
US-08-915-795-3
; Sequence 3, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
US-08-915-795-3

Query Match        100.0%;  Score 46;  DB 3;  Length 325;
Best Local Similarity 100.0%;  Pred. No. 0.97;
Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1  CNEESLIC  8
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Db        117  CNEESLIC  124

RESULT 5
US-08-915-795-5
; Sequence 5, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
US-08-915-795-5

Query Match   100.0%; Score 46; DB 3; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
          ||||||||
Db   146 CNEESLIC 153

RESULT 6
5194596-9
;Patent No. 5194596
; APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES, JOHN
;C.;MITCHELL, RICHARD L.
; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
;GROWTH FACTOR
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/450,883
;   FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 387,545
;   FILING DATE: 27-JUL-1989
;SEQ ID NO:9:
; LENGTH: 120
5194596-9

Query Match   78.3%; Score 36; DB 6; Length 120;
Best Local Similarity 75.0%; Pred. No. 20;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
          ||:||||
Db   60 CNDESLEC 67

RESULT 7
5219739-9
;Patent No. 5219739
; APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES,
;JOHN C.;MITCHELL, RICHARD L.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING BVEGF120 AND
;HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
;VAASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVEGF120 AND HVEGF121
; NUMBER OF SEQUENCES: 40
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/559,041
;   FILING DATE: 27-JUL-1990
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 450,883
;   FILING DATE: 14-DEC-1989
;   APPLICATION NUMBER: 387,545
;   FILING DATE: 27-JUL-1989
;SEQ ID NO:9:
; LENGTH: 120
5219739-9

Query Match   78.3%; Score 36; DB 6; Length 120;
Best Local Similarity 75.0%; Pred. No. 20;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
          ||:||||
Db   60 CNDESLEC 67

RESULT 8
US-09-125-642C-15
; Sequence 15, Application US/09125642C
; Patent No. 6365393
; GENERAL INFORMATION:
;   APPLICANT: BAYER AG
;   TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
;   Their Production and Their Use in Vaccines
;   NUMBER OF SEQUENCES: 18
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Bayer Corporation
;   STREET: 100 Bayer Road
;   CITY: Pittsburgh
;   STATE: Pennsylvania
;   COUNTRY: U.S.A.
;   ZIP: 15205-9741
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/125,642C
;   FILING DATE: 20-Aug-1998
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/EP97/00729,
;   FILING DATE: 17-Feb-97
; INFORMATION FOR SEQ ID NO: 15:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 132 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;   ORGANISM: Parapox ovis
;   STRAIN: D1701 VEGF- Protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-125-642C-15

Query Match   78.3%; Score 36; DB 4; Length 132;
Best Local Similarity 75.0%; Pred. No. 22;
Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CNEESLIC 8
          ||:||||
Db   70 CNDESLEC 77

RESULT 9
US-09-431-888-11
; Sequence 11, Application US/09431888A
; Patent No. 6541008
; GENERAL INFORMATION:
;   APPLICANT: Wise, Lyn M
;   APPLICANT: Mercer, Andrew A
;   APPLICANT: Savory, Loreen J
;   APPLICANT: Fleming, Stephen B
;   APPLICANT: Stacker, Stephen
;   TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
;   TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
;   TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
;   FILE REFERENCE: Sequence Listing for 09/431,833
;   Patent No. 6541008
;   CURRENT APPLICATION NUMBER: US/09/431,888A
;   CURRENT FILING DATE: 1999-11-02
;   EARLIER APPLICATION NUMBER: 60/106,689
;   EARLIER FILING DATE: 1998-11-02
;   EARLIER APPLICATION NUMBER: 60/106,800

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; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 132
;   TYPE: PRT
;   ORGANISM: Orf virus
US-09-431-888-11

Query Match     78.3%;   Score 36;   DB 4;   Length 132;
Best Local Similarity   75.0%;   Pred. No. 22;
Matches    6;   Conservative    1;   Mismatches    1;   Indels    0;   Gaps    0;

Qy    1  CNEESLIC 8
         ||:|||
Db   70  CNDESLEC 77

RESULT 10
US-09-431-888-2
; Sequence 2, Application US/09431888A
; GENERAL INFORMATION:
;  APPLICANT: Wise, Lyn M
;  APPLICANT: Mercer, Andrew A
;  APPLICANT: Savory, Loreen J
;  APPLICANT: Fleming, Stephen B
;  APPLICANT: Stacker, Stephen
;  TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
;  TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
;  TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence Listing for 09/431,833
; Patent No. 6541008
; CURRENT APPLICATION NUMBER: US/09/431,888A
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/106,689
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/106,800
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 133
;   TYPE: PRT
;   ORGANISM: Orf virus
US-09-431-888-2

Query Match     78.3%;   Score 36;   DB 4;   Length 133;
Best Local Similarity   75.0%;   Pred. No. 22;
Matches    6;   Conservative    1;   Mismatches    1;   Indels    0;   Gaps    0;

Qy    1  CNEESLIC 8
         ||:|||
Db   71  CNDESLEC 78

RESULT 11
5194596-17
;Patent No. 5194596
;  APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES, JOHN
;C.;MITCHELL, RICHARD L.
;  TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
;GROWTH FACTOR
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/07/450,883
;  FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 387,545
;  FILING DATE: 27-JUL-1989
;SEQ ID NO:17:
;  LENGTH: 164
5194596-17


Query Match     78.3%;   Score 36;   DB 6;   Length 164;
Best Local Similarity   75.0%;   Pred. No. 27;
Matches    6;   Conservative    1;   Mismatches    1;   Indels    0;   Gaps    0;

Qy    1  CNEESLIC 8
         ||:|||
Db   60  CNDESLEC 67

RESULT 12
5219739-17
;Patent No. 5219739
;  APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES,
;JOHN C.;MITCHELL, RICHARD L.
;  TITLE OF INVENTION: DNA SEQUENCES ENCODING BVEGF120 AND
;HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
;VAASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVEGF120 AND HVEGF121
; NUMBER OF SEQUENCES: 40
; CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/07/559,041
;  FILING DATE: 27-JUL-1990
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 450,883
;  FILING DATE: 14-DEC-1989
;  APPLICATION NUMBER: 387,545
;  FILING DATE: 27-JUL-1989
;SEQ ID NO:17:
;  LENGTH: 164
5219739-17

Query Match     78.3%;   Score 36;   DB 6;   Length 164;
Best Local Similarity   75.0%;   Pred. No. 27;
Matches    6;   Conservative    1;   Mismatches    1;   Indels    0;   Gaps    0;

Qy    1  CNEESLIC 8
         ||:|||
Db   60  CNDESLEC 67

RESULT 13
5219739-18
;Patent No. 5219739
;  APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES,
;JOHN C.;MITCHELL, RICHARD L.
;  TITLE OF INVENTION: DNA SEQUENCES ENCODING BVEGF120 AND
;HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
;VAASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVEGF120 AND HVEGF121
; NUMBER OF SEQUENCES: 40
; CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/07/559,041
;  FILING DATE: 27-JUL-1990
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 450,883
;  FILING DATE: 14-DEC-1989
;  APPLICATION NUMBER: 387,545
;  FILING DATE: 27-JUL-1989
;SEQ ID NO:18:
;  LENGTH: 164
5219739-18

Query Match     78.3%;   Score 36;   DB 6;   Length 164;
Best Local Similarity   75.0%;   Pred. No. 27;
Matches    6;   Conservative    1;   Mismatches    1;   Indels    0;   Gaps    0;

Qy    1  CNEESLIC 8
         ||:|||
Db   60  CNDESLEC 67

RESULT 14
5332671-3
;Patent No. 5332671
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Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 0;

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Qy    1 CNEESLIC 8
        |||| ::|
Db  146 CNEEGVMC 153
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Search completed: September 5, 2004, 10:21:56
Job time : 7.11111 secs

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; APPLICANT: FERRARA, NAPOLEONE;LEUNG, DAVID W.H.
; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
;GROWTH FACTOR AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07/389,722
;     FILING DATE: 04-AUG-1989
; PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 369,424
;     FILING DATE: 21-JUN-1989
;     APPLICATION NUMBER: 351,117
;     FILING DATE: 12-MAY-1989
;SEQ ID NO:3:
;     LENGTH: 190
5332671-3
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Query Match 78.3%; Score 36; DB 6; Length 190;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

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Qy    1 CNEESLIC 8
        ||:||||
Db   86 CNDESLEC 93
```

RESULT 15
US-08-915-795-9
```
; Sequence 9, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: Mouse Lung
US-08-915-795-9
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Query Match 78.3%; Score 36; DB 3; Length 321;
Best Local Similarity 62.5%; Pred. No. 53;

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   September 5, 2004, 09:47:29 ; Search time 8.44444 Seconds
                                        (without alignments)
                                        125.302 Million cell updates/sec

Title:    US-09-761-636A-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11
Scoring table: BLOSUM62
          Gapop 10.0 , Gapext 0.5
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Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Database :  PIR 78:*
          1: pir1:*
          2: pir2:*
          3: pir3:*
          4: pir4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	63.9	151	2	PQ0506	hypothetical prote
2	39	63.9	169	2	A72466	hypothetical prote
3	39	63.9	207	2	I47061	collagenase inhibi
4	39	63.9	925	2	T29311	hypothetical prote
5	39	63.9	1062	2	T46444	hypothetical prote
6	38	62.3	324	2	T31992	hypothetical prote
7	38	62.3	503	2	S62018	probable membrane
8	38	62.3	616	2	T29234	hypothetical prote
9	38	62.3	1829	2	T34239	hypothetical prote
10	37	60.7	184	2	B96814	hypothetical prote
11	37	60.7	527	2	H85135	hypothetical prote
12	37	60.7	583	2	F70592	probable lpqB prot
13	37	60.7	788	2	G64707	cation-transportin
14	37	60.7	788	2	E71813	probable component
15	37	60.7	1787	2	T20160	hypothetical prote
16	36	59.0	165	2	B72727	hypothetical prote
17	36	59.0	174	2	JV0046	hypothetical 18K p
18	36	59.0	261	2	T16392	hypothetical prote
19	36	59.0	533	2	T46975	lysine-tRNA ligase
20	36	59.0	534	2	C64367	hypothetical prote
21	36	59.0	954	2	G71496	hypothetical prote
22	35	57.4	112	2	E72785	hypothetical prote
23	35	57.4	119	2	A59047	phospholipase A2 (
24	35	57.4	207	1	A35685	metalloproteinase
25	35	57.4	207	2	I46964	metalloproteinase
26	35	57.4	296	2	T34460	hypothetical prote
27	35	57.4	302	2	B81696	4-hydroxybenzoate
28	35	57.4	308	2	T29756	hypothetical prote
29	35	57.4	342	2	T25143	hypothetical prote
30	35	57.4	354	2	T31861	hypothetical prote
31	35	57.4	363	2	T02522	origin recognition
32	35	57.4	403	2	C75405	streptomycin biosy
33	35	57.4	410	2	T19995	hypothetical prote
34	35	57.4	457	2	B84725	probable glucosylt
35	35	57.4	537	2	T48599	hypothetical prote
36	35	57.4	756	2	T20109	hypothetical prote
37	35	57.4	790	2	T25095	hypothetical prote
38	35	57.4	970	2	D59435	Gem-interacting pr
39	35	57.4	1099	2	T16283	hypothetical prote
40	35	57.4	3014	1	JC5620	genome polyprotein
41	34.5	56.6	1246	2	T00826	hypothetical prote
42	34.5	56.6	1816	2	A84845	probable ABC trans
43	34	55.7	61	2	C90971	probable lipoprote
44	34	55.7	61	2	H90901	probable lipoprote
45	34	55.7	76	2	JR0003	hypothetical 8.6K

ALIGNMENTS

RESULT 1
PQ0506
hypothetical protein 151 - fowlpox virus (fragment)
N;Alternate names: ORF3 protein
C;Species: fowlpox virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 03-Nov-2000
C;Accession: PQ0506; S27935
R;Ogawa, R.; Calvert, J.G.; Yanagida, N.; Nazerian, K.
J. Gen. Virol. 74, 55-64, 1993
A;Title: Insertional inactivation of a fowlpox virus homologue of the vaccinia virus F12
A;Reference number: JQ1894; MUID:9139784; PMID:8380837
A;Accession: PQ0506
A;Molecule type: DNA
A;Residues: 1-151 <OGA>
A;Cross-references: GB:M88588; NID:g333522; PIDN:AAA47188.1; PID:g333525
A;Note: submitted to the EMBL Data Library, May 1992

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Query Match     63.9%;   Score 39;  DB 2;  Length 151;
Best Local Similarity   50.0%;   Pred. No. 11;
Matches   5;  Conservative   4;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    1 CISVPLTSVP 10
          ||::||:||:|
Db   90 CINIPIDSIP 99
```

RESULT 2
A72466
hypothetical protein APE2372 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: A72466
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: A72466
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <KAW>
A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81385.1; PID:d1045171; PID:g510
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE2372

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Query Match     63.9%;   Score 39;  DB 2;  Length 169;
Best Local Similarity   60.0%;   Pred. No. 12;
Matches   6;  Conservative   6;  Mismatches   2;  Indels   0;  Gaps   0;

Qy    1 CISVPLTSVP 10
          || :|: |||
```

Db   57 CIGIPVASVP 66

RESULT 3
I47061
collagenase inhibitor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 16-Jul-1999
C;Accession: I47061
R;Tanaka, T.; Andoh, N.; Takeya, T.; Sato, B.
Mol. Cell. Endocrinol. 83, 65-71, 1992
A;Title: Differential screening of ovarian cDNA libraries detected the expression of the
A;Reference number: I47061; MUID:9201478; PMID:1312961
A;Accession: I47061
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-207 <TAN>
A;Cross-references: GB;S96211; NID:g247729; PIDN:AAB21865.1; PID:g247730
C;Superfamily: metalloproteinase inhibitor

Query Match   63.9%;   Score 39; DB 2; Length 207;
Best Local Similarity   54.5%;   Pred. No. 15;
  Matches   6; Conservative   1; Mismatches   4; Indels   0; Gaps   0;

Qy   1 CISVPLTSVPC 11
               | ||:|||
Db   150 CTVFPCTSIPC 160

RESULT 4
T29311
hypothetical protein F36D4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29311
R;Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F36D4.
A;Reference number: Z20603
A;Accession: T29311
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-925 <PAU>
A;Cross-references: EMBL:U53181; PIDN:AAA93485.1; GSPDB:GN00023; CESP:F36D4
A;Experimental source: strain Bristol N2; clone F36D4
C;Genetics:
A;Gene: CESP:F36D4.3
A;Map position: 5
A;Introns: 24/3; 56/2; 103/3; 187/1; 387/2; 429/3; 455/3; 516/1; 555/1; 782/2; 882/3

Query Match   63.9%;   Score 39; DB 2; Length 925;
Best Local Similarity   50.0%;   Pred. No. 64;
  Matches   5; Conservative   5; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVPC 11
               :|:||:|:|||
Db   2 VSLPMSNVPC 11

RESULT 5
T46444
hypothetical protein DKFZp434N1427.1 - human
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46444
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: 223032
A;Accession: T46444
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1062 <AAA>
A;Cross-references: EMBL:AL137701

A;Experimental source: adult testis; clone DKFZp434N1427
C;Genetics:
A;Note: DKFZp434N1427.1

Query Match   63.9%;   Score 39; DB 2; Length 1062;
Best Local Similarity   66.7%;   Pred. No. 74;
  Matches   6; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   3 SVPLTSVPC 11
               |:||:||
Db   25 SIPLSSTPC 33

RESULT 6
T31992
hypothetical protein C49D10.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C;Accession: T31992
R;Henkhaus, J.; Wohldmann, P.; Beck, C.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C49D10.
A;Reference number: Z21108
A;Accession: T31992
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-324 <HEN>
A;Cross-references: EMBL:AF016665; PIDN:AAC71178.1; GSPDB:GN00020; CESP:C49D10.3
A;Experimental source: strain Bristol N2; clone C49D10
C;Genetics:
A;Gene: CESP:C49D10.3
A;Map position: 2
A;Introns: 105/1
C;Superfamily: Caenorhabditis hypothetical protein C49G7.2

Query Match   62.3%;   Score 38; DB 2; Length 324;
Best Local Similarity   54.5%;   Pred. No. 34;
  Matches   6; Conservative   1; Mismatches   4; Indels   0; Gaps   0;

Qy   1 CISVPLTSVPC 11
               ||:| ||:||
Db   70 CIGVPYLHLPC 80

RESULT 7
S62018
probable membrane protein YDR539w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D3703.2
C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 19-Apr-2002
C;Accession: S62018
R;Dietrich, F.S.; Mulligan, J.; Allen, E.; Araujo, R.; Aviles, E.; Berno, A.; Carpenter,
H.; Lin, D.; Mosedale, D.; Nakahara, K.; Namath, A.; Oefner, P.; Oh, C.; Petel, F.X.; R
W.
submitted to the EMBL Data Library, December 1995
A;Reference number: S62017
A;Accession: S62018
A;Molecule type: DNA
A;Residues: 1-503 <DIE>
A;Cross-references: EMBL:U43834; NID:g1165292; PID:g1165294; GSPDB:GN00004; MIPS:YDR539
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YDR539w
A;Cross-references: SGD:S0002947
A;Map position: 4R
C;Superfamily: conserved hypothetical protein sll0936
C;Keywords: transmembrane protein #status predicted <TMM>
F;210-226/Domain: transmembrane #status predicted <TMM>

Query Match   62.3%;   Score 38; DB 2; Length 503;
Best Local Similarity   60.0%;   Pred. No. 53;
  Matches   6; Conservative   3; Mismatches   1; Indels   0; Gaps   0;

Qy   2 ISVPLTSVPC 11
          |:||::||||
Db   115 ITVPVSSAPC 124

RESULT 8
T29234
hypothetical protein F55G1.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29234
R;Murray, J.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z20591
A;Accession: T29234
A;Accession: T29234
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-616 <MUR>
A;Cross-references: EMBL:U58750; PIDN:AAB00653.1; GSPDB:GN00022; CESP:F55G1.13
A;Experimental source: strain Bristol N2; clone F55G1
C;Genetics:
A;Gene: CESP:F55G1.13
A;Map position: 4
A;Introns: 98/1; 136/1; 230/1; 256/1; 363/1; 401/1; 443/1; 484/1; 528/2; 551/3

Query Match   62.3%;   Score 38; DB 2; Length 616;
Best Local Similarity   54.5%;   Pred. No. 65;
Matches   6; Conservative   1; Mismatches   4; Indels   0; Gaps   0;

Qy   1 CISVPLTSVPC 11
          |: |||||| ||
Db   362 CVGNPCTSEPC 372

RESULT 9
T34239
hypothetical protein F26F12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34239
R;Wilson, R.; Bentley, D.; Gattung, S.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z21493
A;Accession: T34239
A;Accession: T34239
A;Description: The sequence of C. elegans cosmid F26F12.
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1829 <WIL>
A;Cross-references: EMBL:U55373; PIDN:AAC25894.1; GSPDB:GN00023; CESP:F26F12.7
A;Experimental source: strain Bristol N2; clone F26F12
C;Genetics:
A;Gene: CESP:F26F12.7
A;Map position: 5
A;Introns: 110/3; 441/3; 801/2; 1244/3; 1693/2; 1784/1

Query Match   62.3%;   Score 38; DB 2; Length 1829;
Best Local Similarity   70.0%;   Pred. No. 1.9e+02;
Matches   7; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   1 CISVPLTSVP 10
          | ||| ||
Db   343 CIDPPLTEVP 352

RESULT 10
B96814
hypothetical protein T30F21.11 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96814
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96814
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <STO>
A;Cross-references: GB:AE005173; NID:g4836878; PIDN:AAD30581.1; GSPDB:GN00141
C;Genetics:
A;Gene: T30F21.11
A;Map position: 1

Query Match   60.7%;   Score 37; DB 2; Length 184;
Best Local Similarity   85.7%;   Pred. No. 30;
Matches   6; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   5 PLTSVPC 11
          |||:|||
Db   150 PLTAVPC 156

RESULT 11
H85135
hypothetical protein AT4g12650 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: H85135
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: H85135
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-527 <STO>
A;Cross-references: GB:NC_001268; NID:g7267967; PIDN:CAB78308.1; GSPDB:GN00140
C;Genetics:
A;Gene: AT4g12650
A;Map position: 4

Query Match   60.7%;   Score 37; DB 2; Length 527;
Best Local Similarity   100.0%;   Pred. No. 83;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CISVPLT 7
          |||||||
Db   344 CISVPLT 350

RESULT 12
F70592
probable lpqB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70592
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70592
A;Molecule type: DNA
A;Residues: 1-583 <COL>
A;Cross-references: GB:Z95121; GB:AL123456; NID:g3261742; PIDN:CAB08345.1; PID:e314477;

A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: lpqB

```
Query Match          60.7%;    Score 37;  DB 2;  Length 583;
Best Local Similarity 70.0%;    Pred. No. 92;
Matches     7;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        1 CISVPLTSVP 10
            |||||||||
Db       16 CASVPSTSAP 25
```

RESULT 13
G64707
cation-transporting ATPase, P-type - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 11-Jan-2000
C;Accession: G64707
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
  Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Mckenne,
  son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: G64707
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-788 <TOM>
A;Cross-references: GB:AE000648; GB:AE000511; NID:g2314670; PIDN:AAD08539.1; PID:g2314670
C;Superfamily: Enterococcus copper-transporting ATPase copA; ATPase nucleotide-binding d
F;218-547/Domain: ATPase transduction domain homology <ATT>
F;612-750/Domain: ATPase nucleotide-binding domain homology <ATN>

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Query Match          60.7%;    Score 37;  DB 2;  Length 788;
Best Local Similarity 63.6%;    Pred. No. 1.2e+02;
Matches     7;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        1 CISVPLTSVPC 11
            |||||  | |||
Db      456 CISVLVISCPC 466
```

RESULT 14
E71813
probable component of cation transport for cbb3-type oxidase - Helicobacter pylori (stra
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jan-2000
C;Accession: E71813
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
  ; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: E71813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-788 <ARN>
A;Cross-references: GB:AE001561; GB:AE001439; NID:g4156000; PIDN:AAD06962.1; PID:g4156000
A;Experimental source: strain J99
C;Genetics:
A;Gene: fixI
C;Superfamily: Enterococcus copper-transporting ATPase copA; ATPase nucleotide-binding d
F;612-750/Domain: ATPase nucleotide-binding domain homology <ATN>

```
Query Match          60.7%;    Score 37;  DB 2;  Length 788;
Best Local Similarity 63.6%;    Pred. No. 1.2e+02;
Matches     7;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        1 CISVPLTSVPC 11
            ||||| | ||
```

```
Db      456 CISVLVISCPC 466
```

RESULT 15
T20160
hypothetical protein T14G8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T20160; T24924
R;McMurray, A.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19231
A;Accession: T20160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1787 <WIL>
A;Cross-references: EMBL:Z67881; PIDN:CAA91798.1; GSPDB:GN00028; CESP:T14G8.1
A;Experimental source: clone C52G5
R;Matthews, P.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19955
A;Accession: T24924
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1787 <WI2>
A;Cross-references: EMBL:Z67884; PIDN:CAA91810.1; GSPDB:GN00028; CESP:T14G8.1
A;Experimental source: clone T14G8
C;Genetics:
A;Gene: CESP:T14G8.1
A;Map position: X
A;Introns: 112/3; 453/3; 597/3; 815/2; 1258/3; 1682/2; 1709/3; 1764/1

```
Query Match          60.7%;    Score 37;  DB 2;  Length 1787;
Best Local Similarity 60.0%;    Pred. No. 2.8e+02;
Matches     6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        1 CISVPLTSVP 10
            ||  ||| :|
Db      354 CIDPPLTEIP 363
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Search completed: September 5, 2004, 10:01:17
Job time : 9.44444 secs

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               GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    September  5, 2004, 09:38:39 ; Search time 5 Seconds
                                   (without alignments)
                              114.554 Million cell updates/sec

Title:   US-09-761-636A-7
Perfect score:  61
Sequence:  1 CISVPLTSVPC 11

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:   141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:    141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_42:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	70.5	326	1	VEGD_RAT	O35251 rattus norv
2	43	70.5	354	1	VEGD_HUMAN	O43915 homo sapien
3	43	70.5	358	1	VEGD_MOUSE	P97946 mus musculu
4	39	63.9	207	1	TIM1_PIG	P35624 sus scrofa
5	39	63.9	451	1	V110_FOWPV	P36700 fowlpox vir
6	39	63.9	1723	1	AIM1_HUMAN	Q9y4k1 homo sapien
7	38	62.3	503	1	YD39_YEAST	Q03034 saccharomyc
8	38	62.3	662	1	T9S2_MOUSE	P58021 mus musculu
9	38	62.3	663	1	T9S2_HUMAN	Q99805 homo sapien
10	37	60.7	892	1	CHD3_DROME	O16102 drosophila
11	37	60.7	1787	1	CHD3_CAEEL	Q22516 caenorhabdi
12	36	59.0	65	1	BB12_SCHCO	P78743 schizophyll
13	36	59.0	337	1	C5L2_HUMAN	Q9p296 homo sapien
14	36	59.0	530	1	SYK_METJA	Q57959 methanococc
15	36	59.0	533	1	SYK_METMP	O30522 methanococc
16	36	59.0	613	1	ADAS_TRYBB	O97157 trypanosoma
17	36	59.0	895	1	STNB_MOUSE	Q8bz60 mus musculu
18	36	59.0	905	1	STNB_HUMAN	Q8wxe9 homo sapien
19	35	57.4	77	1	COMA_CONMA	Q9tw19 conus magus
20	35	57.4	207	1	TIM1_BOVIN	P20414 bos taurus
21	35	57.4	207	1	TIM1_SHEEP	P50122 ovis aries
22	35	57.4	296	1	RPC6_CAEEL	P91529 caenorhabdi
23	35	57.4	363	1	ORC2_ARATH	Q38899 arabidopsis
24	35	57.4	756	1	K6PF_CAEEL	Q27483 caenorhabdi
25	35	57.4	773	1	DGR8_HUMAN	Q8wyq5 homo sapien
26	35	57.4	1041	1	TLR8_HUMAN	Q9nr97 homo sapien
27	35	57.4	1077	1	CYA4_MOUSE	Q9wf3 mus musculu
28	34	55.7	76	1	VG06_BPMU	Q38477 bacteriopha
29	34	55.7	120	1	SY23_HUMAN	P55773 homo sapien
30	34	55.7	207	1	TIM1_HORSE	O02722 equus cabal
31	34	55.7	258	1	KPM1_ECOLI	P23889 escherichia
32	34	55.7	258	1	KPM2_ECOLI	P24584 escherichia
33	34	55.7	319	1	LDH_THEMA	P16115 thermotoga
34	34	55.7	323	1	TKRA_ERWHE	P58000 erwinia her
35	34	55.7	327	1	NAS1_HORVU	Q9zqv9 hordeum vul
36	34	55.7	330	1	OBH6_HUMAN	Q8ngc7 homo sapien
37	34	55.7	349	1	YHHT_ECOLI	P37622 escherichia
38	34	55.7	651	1	TDR3_HUMAN	Q9h7e2 homo sapien
39	34	55.7	753	1	TDR6_HUMAN	O60522 homo sapien
40	34	55.7	837	1	MUCL_RAT	P98089 rattus norv
41	34	55.7	1097	1	EX5C_MYCTU	P96921 mycobacteri
42	34	55.7	1233	1	VL1_REOVD	P15024 reovirus (t
43	34	55.7	1426	1	CUT2_MOUSE	P70298 mus musculu
44	34	55.7	1816	1	LMA4_HUMAN	Q16363 homo sapien
45	34	55.7	2142	1	BAT2_HUMAN	P48634 homo sapien

ALIGNMENTS

```
RESULT 1
VEGD_RAT
ID   VEGD_RAT    STANDARD;    PRT;    326 AA.
AC   O35251;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF).
GN   FIGF OR VEGFD.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Yamada Y., Hirata Y., Nezu J., Shimane M.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC       and endothelial cell growth, stimulating their proliferation and
CC       migration and also has effects on the permeability of blood
CC       vessels. May function in the formation of the venous and lymphatic
CC       vascular systems during embryogenesis, and also in the maintenance
CC       of differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-3 (Flt4) receptor (By similarity).
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC       linked by disulfide bonds before secretion. The fully processed
CC       VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC       bound by non-covalent interactions (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF014827; AAB65557.1; -.
DR   HSSP; P15692; 1VPP.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 1.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
```

```
FT   SIGNAL        1     21       POTENTIAL.
FT   PROPEP       22     93       POTENTIAL.
FT   CHAIN        94    210       VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP      211    326       POTENTIAL.
FT   DOMAIN      227    317       4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT                                X(1,3)-C.
FT   REPEAT      227    242       1 (APPROXIMATE).
FT   REPEAT      263    278       2.
FT   REPEAT      282    298       3.
FT   REPEAT      306    317       4 (INCOMPLETE).
FT   DISULFID    116    158       BY SIMILARITY.
FT   DISULFID    147    194       BY SIMILARITY.
FT   DISULFID    151    196       BY SIMILARITY.
FT   DISULFID    141    141       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    150    150       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    160    160       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    190    190       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    292    292       N-LINKED (GLCNAC...) (POTENTIAL).
FT   SEQUENCE    326 AA;  37112 MW;  1261AFA73596C00 CRC64;

Query Match             70.5%;
Best Local Similarity  100.0%;   Score 43;   DB 1;   Length 326;   Pred. No. 1.4;
Matches    9;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy    2  ISVPLTSVP   10
         |||||||||
Db  173  ISVPLTSVP  181


RESULT 2
VEGD_HUMAN
ID   VEGD_HUMAN    STANDARD;    PRT;    354 AA.
AC   O43915;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF).
GN   FIGF OR VEGFD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=97349118; PubMed=9205122;
RA   Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=98140120; PubMed=9479493;
RA   Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA   Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT   "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT   between the PIGA and the GRPR genes.";
RL   Genomics 47:207-216(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98118549; PubMed=9435229;
RA   Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,
RA   Alitalo K., Stacker S.A.;
RT   "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT   tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
RX   MEDLINE=20011413; PubMed=10542248;
RA   Stacker S.A., Stenvers K.L., Caesar C., Vitali A., Domagala T.,
RA   Nice E.C., Roufail S., Simpson R.J., Moritz R., Karpanen T.,
RA   Alitalo K., Achen M.G.;
RT   "Biosynthesis of vascular endothelial growth factor-D involves
RT   proteolytic processing which generates non-covalent homodimers.";
RL   J. Biol. Chem. 274:32127-32136(1999).
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC       and endothelial cell growth, stimulating their proliferation and
CC       migration and also has effects on the permeability of blood
CC       vessels. May function in the formation of the venous and lymphatic
CC       vascular systems during embryogenesis, and also in the maintenance
CC       of differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in lung, heart, small
CC       intestine and fetal lung, and at lower levels in skeletal muscle,
CC       colon, and pancreas.
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC       linked by disulfide bonds before secretion. The fully processed
CC       VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC       bound by non-covalent interactions.
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
```

```
DR   EMBL; D89630; BAA24264.1; -.
DR   EMBL; Y12863; CAA73370.1; -.
DR   EMBL; Y12864; CAA73371.1; -.
DR   EMBL; Y12865; CAA73371.1; JOINED.
DR   EMBL; Y12866; CAA73371.1; JOINED.
DR   EMBL; Y12867; CAA73371.1; JOINED.
DR   EMBL; Y12868; CAA73371.1; JOINED.
DR   EMBL; Y12869; CAA73371.1; JOINED.
DR   EMBL; Y12870; CAA73371.1; JOINED.
DR   EMBL; AJ000185; CAA03942.1; -.
DR   EMBL; BC027948; AAH27948.1; -.
DR   HSSP; P15692; 1VPP.
DR   Genew; HGNC:3708; FIGF.
DR   MIM; 300091; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005161; F:platelet-derived growth factor receptor bin... .; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
```

DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 3.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL   1   21   POTENTIAL.
FT   PROPEP   22   88   OR 99 (IN A MINOR FORM).
FT   CHAIN   89   205   VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP   206   354
FT   DOMAIN   222   318   4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT   X(1,3)-C.
FT   REPEAT   222   237   1 (APPROXIMATE).
FT   REPEAT   258   273   2.
FT   REPEAT   277   293   3.
FT   REPEAT   301   318   4.
FT   DISULFID   111   153   BY SIMILARITY.
FT   DISULFID   142   189   BY SIMILARITY.
FT   DISULFID   146   191   BY SIMILARITY.
FT   DISULFID   136   136   INTERCHAIN (BY SIMILARITY).
FT   DISULFID   145   145   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   155   155   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   185   185   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   287   287   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   354 AA;   40444 MW;   2048D769D735173E CRC64;

Query Match   70.5%; Score 43; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
            |||||||||
Db   168 ISVPLTSVP 176

RESULT 3
VEGD_MOUSE
ID   VEGD_MOUSE   STANDARD;   PRT;   358 AA.
AC   P97946;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF)
GN   FIGF OR VEGFD.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Fibroblast;
RX   MEDLINE=97030254; PubMed=8876195;
RA   Orlandini M., Marconcini L., Ferruzzi R., Oliviero S.;
RT   "Identification of a c-fos-induced gene that is related to the
RT   platelet-derived growth factor/vascular endothelial growth factor
RT   family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=97349118; PubMed=9205122;
RA   Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
RN   [3]
RP   DEVELOPMENTAL STAGE.

RX   MEDLINE=98288130; PubMed=9622638;
RA   Avantaggiato V., Orlandini M., Acampora D., Oliviero S., Simeone A.;
RT   "Embryonic expression pattern of the murine figf gene, a growth factor
RT   belonging to platelet-derived growth factor/vascular endothelial
RT   growth factor family.";
RL   Mech. Dev. 73:221-224(1998).
RN   [4]
RP   RECEPTOR SPECIFICITY.
RX   MEDLINE=21276411; PubMed=11279005;
RA   Baldwin M.E., Catimel B., Nice E.C., Roufail S., Hall N.E.,
RA   Stenvers K.L., Karkkainen M.J., Alitalo K., Stacker S.A., Achen M.G.;
RT   "The specificity of receptor binding by vascular endothelial growth
RT   factor-d is different in mouse and man.";
RL   J. Biol. Chem. 276:19166-19171(2001).
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC   and endothelial cell growth, stimulating their proliferation and
CC   migration and also has effects on the permeability of blood
CC   vessels. May function in the formation of the venous and lymphatic
CC   vascular systems during embryogenesis, and also in the maintenance
CC   of differentiated lymphatic endothelium in adults. Binds and
CC   activates VEGFR-3 (Flt4) receptor.
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in fetal and adult lung.
CC   -!- DEVELOPMENTAL STAGE: Expressed in a dynamic pattern in several
CC   body structures and organs of the embryo such as limb buds,
CC   acoustic ganglion, teeth, heart, anterior pituitary as well as
CC   lung and kidney mesenchyme, liver, derma, and periosteum of the
CC   vertebral column.
CC   -!- INDUCTION: By the transcription factor c-fos.
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC   variety of processed secreted forms with increased activity toward
CC   VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC   linked by disulfide bonds before secretion. The fully processed
CC   VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC   bound by non-covalent interactions (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   --
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; X99572; CAA67892.1; -.
DR   EMBL; D89628; BAA14002.1; -.
DR   HSSP; P15692; 1VPP.
DR   PMMA-2DPAGE; P97946; -.
DR   MGD; MGI:108037; Figf.
DR   GO; GO:0005576; C:extracellular; IDA.
DR   GO; GO:0008083; F:growth factor activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0008283; P:cell proliferation; IDA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 2.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL   1   21   POTENTIAL.
FT   PROPEP   22   93   POTENTIAL.
FT   CHAIN   94   210   VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP   211   358   POTENTIAL.
FT   DOMAIN   227   323   4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT   X(1,3)-C.
FT   REPEAT   227   242   1 (APPROXIMATE).
FT   REPEAT   263   278   2.

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FT   REPEAT       282    298       3.
FT   REPEAT       306    323       4.
FT   DISULFID     116    158       BY SIMILARITY.
FT   DISULFID     147    194       BY SIMILARITY.
FT   DISULFID     151    196       BY SIMILARITY.
FT   DISULFID     141    141       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     150    150       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     160    160       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     190    190       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     292    292       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE  358 AA;  40908 MW;  6636B17FBF07037C CRC64;

Query Match
Best Local Similarity   70.5%;  DB 1;  Length 358;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      2   ISVPLTSVP     10
            |||||||||
Db    173   ISVPLTSVP    181

RESULT 4
TIM1_PIG
ID   TIM1_PIG       STANDARD;       PRT;   207 AA.
AC   P35624; Q9TT83; Q9TTB9;
DT   01-JUN-1994 (Rel. 29, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN   TIMP1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=92201478; PubMed=1312961;
RA   Tanaka T., Andoh N., Takeya T., Sato E.;
RT   "Differential screening of ovarian cDNA libraries detected the
RT   expression of the porcine collagenase inhibitor gene in functional
RT   corpora lutea.";
RL   Mol. Cell. Endocrinol. 83:65-71(1992).
RN   [2]
RP   SEQUENCE OF 34-195 FROM N.A.
RA   Wang J.Y., Baer A.E., Kraus V.B., Setton L.A.;
RT   "Gene expression level of mmp3 and Timp1 in intervertebral disc.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 37-144 FROM N.A.
RC   TISSUE=Skin;
RA   Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
RT   "Cloning and sequencing of porcine TIMPs.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC       and irreversibly inactivates them.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: The activity of TIMP1 is dependent on the presence of
CC       disulfide bonds.
CC   -!- SIMILARITY: Belongs to the TIMP family.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ----
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CC   ----
DR   EMBL; S96211; AAB21865.1; -.
DR   EMBL; AF201726; AAF24348.1; -.
DR   EMBL; AF156029; AAF17354.1; -.
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DR   PIR; I47061; I47061.
DR   HSSP; P01033; 1UEA.
DR   InterPro; IPR001820; TIMP.
DR   InterPro; IPR008993; TIMP_like.
DR   Pfam; PF00965; TIMP; 1.
DR   SMART; SM00206; NTR; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
KW   Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW   Signal.
FT   SIGNAL         1     23       BY SIMILARITY.
FT   CHAIN         24    207       METALLOPROTEINASE INHIBITOR 1.
FT   DOMAIN        24    147       NTR.
FT   DISULFID      24     93       BY SIMILARITY.
FT   DISULFID      26    122       BY SIMILARITY.
FT   DISULFID      36    147       BY SIMILARITY.
FT   DISULFID     150    197       BY SIMILARITY.
FT   DISULFID     155    160       BY SIMILARITY.
FT   DISULFID     168    189       BY SIMILARITY.
FT   CARBOHYD      53     53       N-LINKED (GLCNAC...).
FT   CARBOHYD     101    101       N-LINKED (GLCNAC...).
FT   CONFLICT      34     34       A -> P (IN REF. 2).
FT   CONFLICT      37     37       S -> N (IN REF. 3).
FT   CONFLICT      41     41       V -> F (IN REF. 2).
FT   CONFLICT      59     59       K -> Q (IN REF. 1).
FT   CONFLICT      86     86       T -> A (IN REF. 3).
FT   CONFLICT     141    142       EI -> KT (IN REF. 3).
SQ   SEQUENCE  207 AA;  23098 MW;  B04895846EB56BD0 CRC64;

Query Match
Best Local Similarity   63.9%;  Score 39;  DB 1;  Length 207;
Matches    6;  Conservative   1;  Mismatches   4;  Indels   0;  Gaps   0;

Qy      1   CISVPLTSVPC     11
            | |||.||:||
Db    150   CTVFPCTSIPC    160

RESULT 5
V110_FOWPV
ID   V110_FOWPV      STANDARD;       PRT;   451 AA.
AC   P36700; Q9J5B2;
DT   01-JUN-1994 (Rel. 29, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Protein FPV110.
GN   FPV110.
OS   Fowlpox virus (FPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Avipoxvirus.
OX   NCBI_TaxID=10261;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20193820; PubMed=10729156;
RA   Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT   "The genome of fowlpox virus.";
RL   J. Virol. 74:3815-3831(2000).
RN   [2]
RP   SEQUENCE OF 1-151 FROM N.A.
RX   MEDLINE=93139784; PubMed=8380837;
RA   Ogawa R., Calvert J.G., Yanagida N., Nazerian K.;
RT   "Insertional inactivation of a fowlpox virus homologue of the
RT   vaccinia virus F12L gene inhibits the release of enveloped virions.";
RL   J. Gen. Virol. 74:55-64(1993).
CC   -!- SIMILARITY: BELONGS TO THE POXVIRUSES F11 FAMILY.
CC   ----
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CC   or send an email to license@isb-sib.ch).
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CC   -------
DR   EMBL; AF198100; AAF44454.1; -.
DR   EMBL; M88588; AAA47188.1; -.
DR   PIR; PQ0506; PQ0506.
DR   InterPro; IPR007027; Pox_F11.
DR   Pfam; PF04943; Pox_F11; 1.
SQ   SEQUENCE   451 AA;  52010 MW;  66462EA83D3A331 CRC64;

Query Match             63.9%;  Score 39;  DB 1;  Length 451;
Best Local Similarity   50.0%;  Pred. No. 11;
Matches    5;  Conservative    4;  Mismatches    4;  Indels    1;  Gaps    0;

Qy          1 CISVPLTSVP 10
              |:|::|:|
Db         90 CINIPIDSIP 99


RESULT 6
AIM1_HUMAN
ID   AIM1_HUMAN     STANDARD;      PRT;   1723 AA.
AC   Q9Y4K1; O00296;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Absent in melanoma 1 protein.
GN   AIM1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=liver;
RX   MEDLINE=97250519; PubMed=9096375;
RA   Ray M.E., Wistow G., Su Y.A., Meltzer P.S., Trent J.M.;
RT   "AIM1, a novel non-lens member of the betagamma-crystallin
RT   superfamily, is associated with the control of tumorigenicity in human
RT   malignant melanoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:3229-3234(1997).
-!- FUNCTION: May function as suppressor of malignant melanoma. It may
    exert its effects through interactions with the cytoskeleton.
-!- SIMILARITY: Belongs to the beta/gamma-crystallin family.
-!- SIMILARITY: Contains 12 beta/gamma crystallin 'Greek key' domains.
-!- SIMILARITY: Contains 1 ricin B-type lectin domain.
CC   -------
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CC   or send an email to license@isb-sib.ch).
CC   -------
DR   EMBL; U83116; AAB53792.1; -.
DR   EMBL; U83115; AAB53791.1; -.
DR   HSSP; P02526; 1GAM.
DR   Genew; HGNC:356; AIM1.
DR   MIM; 601797; -.
DR   InterPro; IPR001064; Crystallin.
DR   InterPro; IPR000772; RicinB_lectin.
DR   InterPro; IPR008997; RicinB_like.
DR   Pfam; PF00030; crystall; 6.
DR   Pfam; PF00652; Ricin_B_lectin; 3.
DR   PRINTS; PR01367; BGCRYSTALLIN.
DR   SMART; SM00458; RICIN; 1.
DR   SMART; SM00247; XTALbg; 1.
DR   PROSITE; PS00915; CRYSTALLIN_BETAGAMMA; 12.
DR   PROSITE; PS50231; RICIN_B_LECTIN; 1.
KW   Repeat; Lectin.
FT   DOMAIN     1022   1061    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 1.
FT   DOMAIN     1062   1117    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 2.
FT   DOMAIN     1123   1163    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 3.
FT   DOMAIN     1164   1206    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 4.
FT   DOMAIN     1218   1270    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 5.
FT   DOMAIN     1271   1313    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 6.
FT   DOMAIN     1319   1361    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 7.
FT   DOMAIN     1362   1404    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 8.
FT   DOMAIN     1415   1452    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 9.
FT   DOMAIN     1453   1496    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 10.
FT   DOMAIN     1502   1542    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 11.
FT   DOMAIN     1543   1584    BETA/GAMMA CRYSTALLIN 'GREEK KEY' 12.
FT   DOMAIN     1586   1719    RICIN B-TYPE LECTIN.
SQ   SEQUENCE   1723 AA;  188646 MW;  7E50F681A627FB09 CRC64;

Query Match             63.9%;  Score 39;  DB 1;  Length 1723;
Best Local Similarity   45.5%;  Pred. No. 45;
Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CISVPLTSVPC 11
              |:|::|:|
Db        481 CVQSPISSFPC 491


RESULT 7
YD39_YEAST
ID   YD39_YEAST     STANDARD;      PRT;    503 AA.
AC   Q03034;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical 56.2 kDa protein in PAD1-YRF1 intergenic region.
GN   YDR539W OR D3703.2.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,
RA   Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA   Hunicke-Smith S., Hyman R., Komp C., Kashkari D., Lew H., Lin D.,
RA   Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
RA   Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA   Winant A., Yelton M., Botstein D., Davis R.W.;
RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ubiD family.
CC   -------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------
DR   EMBL; U43834; AAB64981.1; -.
DR   PIR; S62018; S62018.
DR   GermOnline; 141031; -.
DR   SGD; S0002947; YDR539W.
DR   InterPro; IPR002830; carboxylyase.
DR   Pfam; PF01977; UbiD; 1.
DR   TIGRFAMs; TIGR00148; TIGR00148; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   503 AA;  56164 MW;  379B1931993DB84F CRC64;

Query Match             60.0%;  Score 38;  DB 1;  Length 503;
Best Local Similarity   62.3%;  Pred. No. 18;
Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ISVPLTSVPC 11
              ||:||:|| |
Db        115 ITVPVSSAPC 124


RESULT 8
T9S2_MOUSE
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ID   T9S2_MOUSE     STANDARD;      PRT;    662 AA.
AC   P58021;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Transmembrane 9 superfamily protein member 2 precursor.
GN   TM9SF2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Moore K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan F., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: In the intracellular compartments, may function as a
CC       channel or small molecule transporter (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endosome
CC       (Probable).
CC   -!- SIMILARITY: Belongs to the nonaspanin (TM9SF) family.
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; BC003862; AAH03862.1; -.
DR   MGD; MGI:1915309; TM9sf2.
DR   InterPro; IPR004240; EMP70.
DR   Pfam; PF02990; EMP70; 1.
KW   Signal; Transmembrane.
FT   SIGNAL        1     28
FT   CHAIN        29    662       TRANSMEMBRANE 9 SUPERFAMILY PROTEIN
FT                                MEMBER 2.
FT   DOMAIN       29    299       LUMENAL (POTENTIAL).
FT   TRANSMEM    300    320       POTENTIAL.
FT   DOMAIN      321    373       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    374    394       POTENTIAL.
FT   DOMAIN      395    397       LUMENAL (POTENTIAL).
FT   TRANSMEM    398    418       POTENTIAL.
FT   DOMAIN      419    436       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    437    457       POTENTIAL.
FT   DOMAIN      458    465       LUMENAL (POTENTIAL).
FT   TRANSMEM    466    486       POTENTIAL.
FT   DOMAIN      487    521       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    522    542       POTENTIAL.
FT   DOMAIN      543    553       LUMENAL (POTENTIAL).
FT   TRANSMEM    554    574       POTENTIAL.
FT   DOMAIN      575    590       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    591    611       POTENTIAL.
FT   DOMAIN      612    630       LUMENAL (POTENTIAL).
FT   TRANSMEM    631    651       POTENTIAL.
FT   DOMAIN      652    662       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   662 AA;  75329 MW;  85F113A5D21733E7 CRC64;

Query Match             62.3%;  Score 38;  DB 1;  Length 662;
Best Local Similarity   77.8%;             Pred. No. 25;
Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1 CISVPLTSV 9
          |||||||:
Db  478 CISVPLTFI 486


RESULT 9
T9S2_HUMAN
ID   T9S2_HUMAN     STANDARD;      PRT;    663 AA.
AC   Q99805;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Transmembrane 9 superfamily protein member 2 precursor (p76).
GN   TM9SF2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98398453; PubMed=9729438;
RA   Schimmoeller F., Diaz E., Muehlbauer B., Pfeffer S.R.;
RT   "Characterization of a 76 kDa endosomal, multispanning membrane
RT   protein that is highly conserved throughout evolution.";
RL   Gene 216:311-318(1998).
CC   -!- FUNCTION: In the intracellular compartments, may function as a
CC       channel or small molecule transporter.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endosome
CC       (Probable).
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed. Especially abundant in
CC       pancreas, highly expressed in kidney, lower levels in heart,
CC       brain, skeletal muscle and placenta. Lowest expression in lung and
CC       liver.
CC   -!- SIMILARITY: Belongs to the nonaspanin (TM9SF) family.
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; U81006; AAB38973.1; -.
DR   Genew; HGNC:11865; TM9SF2.
DR   MIM; 604678; -.
DR   GO; GO:0005768; C:endosome; TAS.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0006810; P:transport; TAS.
DR   InterPro; IPR004240; EMP70.
DR   Pfam; PF02990; EMP70; 1.
KW   Signal; Transmembrane.
FT   SIGNAL        1     28
FT   CHAIN        29    663       TRANSMEMBRANE 9 SUPERFAMILY PROTEIN
FT                                MEMBER 2.
FT   DOMAIN       29    300       LUMENAL (POTENTIAL).
FT   TRANSMEM    301    321       POTENTIAL.
FT   DOMAIN      322    374       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    375    395       POTENTIAL.
FT   DOMAIN      396    398       LUMENAL (POTENTIAL).
FT   TRANSMEM    399    419       POTENTIAL.
FT   DOMAIN      420    437       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    438    458       POTENTIAL.
FT   DOMAIN      459    466       LUMENAL (POTENTIAL).
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FT   TRANSMEM    467    487       POTENTIAL.
FT   DOMAIN      488    522       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    523    543       POTENTIAL.
FT   DOMAIN      544    554       LUMENAL (POTENTIAL).
FT   TRANSMEM    555    575       POTENTIAL.
FT   DOMAIN      576    591       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    592    612       POTENTIAL.
FT   DOMAIN      613    631       LUMENAL (POTENTIAL).
FT   TRANSMEM    632    652       POTENTIAL.
FT   DOMAIN      653    663       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   663 AA;   75775 MW;   C21A4D224534734D CRC64;

Query Match             62.3%;   Score 38;   DB 1;   Length 663;
Best Local Similarity   77.8%;   Pred. No. 25;
Matches    7;   Conservative   1;   Mismatches   1;   Indels   0;   Gaps   0;

Qy        1  CISVPLTSV  9
             ||||||| :
Db      479  CISVPLTFI  487


RESULT 10
CHD3_DROME
ID   CHD3_DROME   STANDARD;   PRT;   892 AA.
AC   O16102; Q8SYJ8; Q9VVZ3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Chromodomain helicase-DNA-binding protein 3.
GN   CHD3 OR CG9594.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   REVISIONS.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley; TISSUE=Embryo;
RX   MEDLINE=22426066; PubMed=12537569;
RA   Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA   George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA   Rubin G.M., Celniker S.E.;
RT   "A Drosophila full-length cDNA resource.";
RL   Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
RN   [4]
RP   SEQUENCE OF 1-812 FROM N.A.
RX   MEDLINE=97470991; PubMed=9326634;
RA   Woodage T., Basrai M.A., Baxevanis A.D., Hieter P., Collins F.S.;
RT   "Characterization of the CHD family of proteins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:11472-11477(1997).
CC   -!- FUNCTION: Possible transcription activator (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
CC   -!- SIMILARITY: Contains 2 chromo domains.
CC   -!- SIMILARITY: Contains 1 PHD-type zinc finger.
CC   -!- CAUTION: Ref.3 sequence differs from that shown due to a stop
CC       codon in position 628 and a frameshift in position 720.
CC   -!- CAUTION: Ref.4 sequence differs from that shown due to cloning
CC       artefacts.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AE003517; AAF49162.2; -.
DR   EMBL; AY071503; AAL49125.1; ALT_FRAME.
DR   EMBL; AF007780; AAB87384.1; ALT_SEQ.
DR   FlyBase; FBgn0023395; Chd3.
DR   GO; GO:0005634; C:nucleus; ISS.
DR   GO; GO:0003682; F:chromatin binding; ISS.
DR   GO; GO:0004386; F:helicase activity; ISS.
DR   GO; GO:0006333; P:chromatin assembly/disassembly; NAS.
DR   InterPro; IPR000953; Chromo.
DR   InterPro; IPR001410; DEAD.
DR   InterPro; IPR002464; DEAH_box.
DR   InterPro; IPR001650; Helicase_C.
DR   InterPro; IPR000330; SNF2_N.
DR   InterPro; IPR001965; Znf_PHD.
DR   Pfam; PF00271; helicase_C; 1.
DR   Pfam; PF00628; PHD; 1.
DR   Pfam; PF00176; SNF2_N; 1.
DR   SMART; SM00298; CHROMO; 2.
DR   SMART; SM00487; DEXDc; 1.
DR   SMART; SM00490; HELICc; 1.
DR   SMART; SM00249; PHD; 1.
DR   PROSITE; PS00598; CHROMO_1; FALSE_NEG.
DR   PROSITE; PS50013; CHROMO_2; 2.
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DR   PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
DR   PROSITE; PS01359; ZF_PHD_1; 1.
DR   PROSITE; PS50016; ZF_PHD_2; 1.
KW   DNA-binding; ATP-binding; Helicase; Nuclear protein; Repeat;
KW   Transcription regulation; Activator; Antigen; Zinc-finger.
FT   ZN_FING     35     82    PHD-TYPE.
FT   DOMAIN      84    156    CHROMO 1.
FT   DOMAIN     179    240    CHROMO 2.
FT   NP_BIND    292    299    ATP (POTENTIAL).
FT   SITE       409    412    DEAH BOX.
FT   CONFLICT   617    617    V -> I (IN REF 4).
SQ   SEQUENCE    892 AA;  103021 MW;  E11DF7F65A1F6D6D CRC64;

Query Match             60.7%;  Score 37;  DB 1;  Length 892;
Best Local Similarity   60.0%;  Pred. No. 52;
Matches   6;  Conservative   2;  Mismatches   2;  Indels   2;  Gaps   0;

Qy       1 CISVPLTSVP 10
            |:| ||| :|
Db      61 CLSPPLKSIP 70


RESULT 11
CHD3_CAEEL
ID   CHD3_CAEEL      STANDARD;       PRT;   1787 AA.
AC   Q22516; Q18794;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Chromodomain helicase-DNA-binding protein 3 homolog (CHD-3).
GN   CHD-3 OR T14G8.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20530482; PubMed=11076750;
RA   von Zelewsky T., Palladino F., Brunschwig K., Tobler H., Hajnal A.,
RA   Mueller F.;
RT   "The C. elegans Mi-2 chromatin-remodelling proteins function in vulval
RT   cell fate determination.";
RL   Development 127:5277-5284(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Matthews P., McMurray A.;
RL   Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Chromatin-remodelling protein that function in vulval
CC       cell fate determination.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
CC   -!- SIMILARITY: Contains 2 PHD-type zinc fingers.
CC   -!- SIMILARITY: Contains 2 chromo domains.
CC   -------------------------------------------------------------
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CC   -------------------------------------------------------------
DR   EMBL; AF308444; AAG29837.1; -.
DR   EMBL; Z67844; CAA91810.1; -.
DR   EMBL; Z67881; CAA91810.1; JOINED.
DR   EMBL; Z67881; CAA91798.1; -.
DR   EMBL; Z67884; CAA91798.1; JOINED.
DR   PIR; T20160; T20160.
DR   WormPep; T14G8.1; CE03657.
DR   InterPro; IPR000953; Chromo.
DR   InterPro; IPR001410; DEAD.
DR   InterPro; IPR002464; DEAH_box.
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DR   InterPro; IPR001650; Helicase_C.
DR   InterPro; IPR000330; SNF2_N.
DR   InterPro; IPR001965; Znf_PHD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00385; chromo; 1.
DR   Pfam; PF00271; helicase_C; 1.
DR   Pfam; PF00628; PHD; 2.
DR   Pfam; PF00176; SNF2_N; 1.
DR   SMART; SM00298; CHROMO; 2.
DR   SMART; SM00487; DEXDc; 1.
DR   SMART; SM00490; HELICc; 1.
DR   SMART; SM00249; PHD; 2.
DR   SMART; SM00184; RING; 2.
DR   PROSITE; PS00598; CHROMO_1; FALSE_NEG.
DR   PROSITE; PS50013; CHROMO_2; 1.
DR   PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
DR   PROSITE; PS01359; ZF_PHD_1; 2.
DR   PROSITE; PS50016; ZF_PHD_2; 2.
KW   Chromatin regulator; Nuclear protein; Repeat; Helicase; DNA-binding;
KW   ATP-binding; Zinc-finger.
FT   DOMAIN      59     62    POLY-LYS.
FT   ZN_FING    265    312    PHD-TYPE 1.
FT   ZN_FING    328    375    PHD-TYPE 2.
FT   DOMAIN     373    476    CHROMO 1.
FT   DOMAIN     501    583    CHROMO 2.
FT   DOMAIN    1287   1291    POLY-ARG.
FT   NP_BIND    641    648    ATP (POTENTIAL).
FT   SITE       763    766    DEAH BOX.
SQ   SEQUENCE   1787 AA;  205254 MW;  1EFCE1FBECE59740 CRC64;

Query Match             60.7%;  Score 37;  DB 1;  Length 1787;
Best Local Similarity   60.0%;  Pred. No. 1.1e+02;
Matches   6;  Conservative   1;  Mismatches   3;  Indels   0;  Gaps   0;

Qy       1 CISVPLTSVP 10
            || ||| :|
Db     354 CIDPPLTEIP 363


RESULT 12
BB12_SCHCO
ID   BB12_SCHCO      STANDARD;       PRT;     65 AA.
AC   P78743;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Mating-type pheromone BBP1(2) precursor.
GN   BBP1(2).
OS   Schizophyllum commune (Bracket fungus).
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Agaricales; Schizophyllaceae; Schizophyllum.
OX   NCBI_TaxID=5334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CBS 340.81 / UVM 4-40;
RX   MEDLINE=97321284; PubMed=9178005;
RA   Vaillancourt L.J., Raudaskoski M., Specht C.A., Raper C.A.;
RT   "Multiple genes encoding pheromones and a pheromone receptor define
RT   the B beta 1 mating-type specificity in Schizophyllum commune.";
RL   Genetics 146:541-551(1997).
CC   -!- FUNCTION: Activates B-regulated development.
CC   -------------------------------------------------------------
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CC   -------------------------------------------------------------
DR   EMBL; U74495; AAB41860.1; -.
KW   Prenylation; Lipoprotein; Pheromone.
FT   PROPEP      1      ?     POTENTIAL.
```

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FT   PEPTIDE        ?     62       MATING-TYPE PHEROMONE BBP1(2).
FT   PROPEP        63     65       REMOVED IN MATURE FORM (POTENTIAL).
FT   LIPID         62     62       S-farnesyl cysteine (Potential).
SQ   SEQUENCE      65 AA;  6780 MW;  3341013317AD6065 CRC64;

Query Match                     59.0%;  Score 36;  DB 1;  Length 65;
Best Local Similarity           66.7%;  Pred. No. 4.8;
Matches        6; Conservative   0; Mismatches  3; Indels  0;  Gaps  0;

Qy      3 SVPLTSVPC 11
          |  |||||||
Db     42 SAPLTBAPC 50


RESULT 13
C5L2_HUMAN
ID   C5L2_HUMAN     STANDARD;       PRT;    337 AA.
AC   Q9P296;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   C5a anaphylatoxin chemotactic receptor C5L2.
GN   GPR77 OR C5L2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Ohno M., Hirata T., Enomoto M., Araki T., Sato K., Ishimaru H.,
RA   Takahashi T.A.;
RT   "A putative chemoattractant receptor, C5L2 is expressed in granulocyte
RT   and immature dendritic cells, but mature dendritc cells.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21105913; PubMed=11165367;
RA   Lee D.K., George S.R., Cheng R., Nguyen T., Liu Y., Brown M.,
RA   Lynch K.R., O'Dowd B.F.;
RT   "Identification of four novel human G protein-coupled receptors
RT   expressed in the brain.";
RL   Brain Res. Mol. Brain Res. 86:13-22(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT   "cDNA clones of human proteins involved in signal transduction
RT   sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   FUNCTION.
RC   TISSUE=Brain;
RX   MEDLINE=21850712; PubMed=11773063;
RA   Cain S.A., Monk P.N.;
RT   "The orphan receptor C5L2 has high affinity binding sites for
RT   complement fragments C5a and C5a des Arg(74).";
RL   J. Biol. Chem. 277:7165-7169(2002).
CC   -!- FUNCTION: Receptor for the chemotactic and inflammatory peptide
CC       anaphylatoxin C5a, C4a and C3a and their des arginated
CC       derivatives. Couples weakly to Gi-mediated signaling pathways.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Frontal cortex, hippocampus, hypothalamus,
CC       pons and liver.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -------------------------------------------------------------------
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CC   -------------------------------------------------------------------
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DR   EMBL; AB038237; BAA95414.1; -.
DR   EMBL; AF317655; AAK12640.1; -.
DR   EMBL; AY268430; AAP23197.1; -.
DR   Genew; HGNC:4527; GPR77.
DR   GO; GO:0016526; F:G-protein coupled receptor activity, unknow. ..; NAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     38       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     39     61       1 (POTENTIAL).
FT   DOMAIN       62     72       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     73     95       2 (POTENTIAL).
FT   DOMAIN       96    114       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    115    137       3 (POTENTIAL).
FT   DOMAIN      138    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    150    172       4 (POTENTIAL).
FT   DOMAIN      173    202       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    203    225       5 (POTENTIAL).
FT   DOMAIN      226    237       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    238    260       6 (POTENTIAL).
FT   DOMAIN      261    274       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    275    294       7 (POTENTIAL).
FT   DOMAIN      295    337       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      3      3       N-LINKED (GLCNAC...) (POTENTIAL).
FT   DISULFID    107    186       BY SIMILARITY.
SQ   SEQUENCE    337 AA;  36080 MW;  53AF1B129FE8FF6 CRC64.

Query Match                     59.0%;  Score 36;  DB 1;  Length 337;
Best Local Similarity           50.0%;  Pred. No. 28;
Matches        5; Conservative   4; Mismatches  4; Indels  1;  Gaps  0;

Qy      1 CISVPLTSVP 10
          |:|:|:: :||
Db     84 CLSLPILAVP 93


RESULT 14
SYK_METJA
ID   SYK_METJA      STANDARD;       PRT;    530 AA.
AC   Q57959;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
GN   LYSS OR MJ0539.
OS   Methanococcus jannaschii.
OC   Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC   Methanocaldococcaceae; Methanocaldococcus.
OX   NCBI_TaxID=2190;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX   MEDLINE=96337999; PubMed=8688087;
RA   Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA   Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA   Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA   Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA   Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA   Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA   Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA   Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT   "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT   jannaschii.";
RL   Science 273:1058-1073(1996).
CC   -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
CC       + L-lysyl-tRNA(Lys).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC   -------------------------------------------------------------------
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CC ------
DR EMBL; U67503; AAB98532.1; -.
DR TIGR; MJ0539; -.
DR HAMAP; MF_00177; -; 1.
DR InterPro; IPR002904; Lys_tRNA-synt_1c.
DR InterPro; IPR008925; tRNA-synt_bind.
DR InterPro; IPR001412; tRNA-synt_I.
DR Pfam; PF01921; tRNA-synt_1f; 1.
DR TIGRFAMs; TIGR00467; lysS_arch; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE   28   36   "HIGH" REGION.
FT SITE   278   282   "KMSKS" REGION.
SQ SEQUENCE   530 AA; 61921 MW; 5811837C8A349E9C CRC64;

Query Match   59.0%; Score 36; DB 1; Length 530;
  Best Local Similarity   50.0%; Pred. No. 46;
  Matches   5; Conservative   3; Mismatches   2; Indels   0; Gaps   0;

Qy   2 ISVPLTSVPC 11
              |:||:.:||
Db   84 IGMPLSEIPC 93

RESULT 15
SYK_METMP
ID   SYK_METMP   STANDARD;   PRT;   533 AA.
AC   O30522;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS).
GN   LYSS.
OS   Methanococcus maripaludis.
OC   Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC   Methanococcaceae; Methanococcus.
OX   NCBI_TaxID=39152;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-22.
RC   STRAIN=JJ;
RX   MEDLINE=98016282; PubMed=9353192;
RA   Ibba M., Morgan S., Curnow A.W., Pridmore D.R., Vothknecht U.C.,
RA   Gardner W., Lin W., Woese C.R., Soell D.;
RT   "A euryarchaeal lysyl-tRNA synthetase: resemblance to class I
RT   synthetases.";
RL   Science 278:1119-1122(1997).
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=20570460; PubMed=11121028;
RA   Soell D., Becker H.D., Plateau P., Blanquet S., Ibba M.;
RT   "Context-dependent anticodon recognition by class I lysyl-tRNA
RT   synthetases.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:14224-14228(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
CC   + L-lysyl-tRNA(Lys).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- MISCELLANEOUS: Able to charge E.coli tRNA(Lys) in vitro.
CC   -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC   ------
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CC   ------
DR EMBL; AF009824; AAB87410.1; -.
DR PIR; T46975; T46975.
DR HAMAP; MF_00177; -; 1.
DR InterPro; IPR002904; Lys_tRNA-synt_1c.
DR InterPro; IPR008925; tRNA-synt_bind.
DR InterPro; IPR001412; tRNA-synt_I.
DR Pfam; PF01921; tRNA-synt_1f; 1.
DR TIGRFAMs; TIGR00467; lysS_arch; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SITE   28   36   "HIGH" REGION.
FT SITE   278   282   "KMSKS" REGION.
FT CONFLICT   11   11   I -> L (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE   533 AA; 61273 MW; 007FAB68A57A0AC2 CRC64;

Query Match   59.0%; Score 36; DB 1; Length 533;
  Best Local Similarity   50.0%; Pred. No. 46;
  Matches   5; Conservative   3; Mismatches   2; Indels   0; Gaps   0;

Qy   2 ISVPLTSVPC 11
              |:||:.:||
Db   84 IGMPLSEIPC 93

Search completed: September 5, 2004, 09:56:04
Job time : 7 secs

OM protein - protein search, using sw model

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Run on: September 5, 2004, 09:46:09 ; Search time 24.8889 Seconds
                (without alignments)
                139.448 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_25:*
          1:   sp_archea:*
          2:   sp_bacteria:*
          3:   sp_fungi:*
          4:   sp_human:*
          5:   sp_invertebrate:*
          6:   sp_mammal:*
          7:   sp_mhc:*
          8:   sp_organelle:*
          9:   sp_phage:*
         10:   sp_plant:*
         11:   sp_rodent:*
         12:   sp_virus:*
         13:   sp_vertebrate:*
         14:   sp_unclassified:*
         15:   sp_rvirus:*
         16:   sp_bacteriap:*
         17:   sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	70.5	122	6	Q9GLX1	Q9glx1 bos taurus
2	43	70.5	252	13	Q8QGD7	Q8qgd7 gallus gall
3	43	70.5	326	11	Q91ZE4	Q91ze4 rattus norv
4	42	68.9	348	5	Q9GUB7	Q9gub7 caenorhabdi
5	41	67.2	118	11	Q8C7W1	Q8c7w1 mus musculu
6	40	65.6	208	5	Q9NF93	Q9nf93 leishmania
7	40	65.6	474	11	Q8VIA1	Q8via1 mus musculu
8	40	65.6	782	11	Q8VDF2	Q8vdf2 mus musculu
9	40	65.6	782	11	Q9Z1H6	Q9z1h6 mus musculu
10	39	63.9	169	17	Q9Y9B5	Q9y9b5 aeropyrum p
11	39	63.9	318	12	Q9PY69	Q9py69 soybean mos
12	39	63.9	366	16	Q7U7P2	Q7u7p2 synechococc
13	39	63.9	386	16	Q7V6T2	Q7v6t2 prochloroco
14	39	63.9	500	4	Q8NA51	Q8na51 homo sapien
15	39	63.9	661	10	Q9XGQ5	Q9xgq5 oryza sativ
16	39	63.9	707	11	Q8BW61	Q8bw61 mus musculu
17	39	63.9	737	11	Q8BW83	Q8bw83 mus musculu
18	39	63.9	925	6	Q8HXK6	Q8hxk6 macaca fasc
19	39	63.9	1062	4	Q9NSW2	Q9nsw2 homo sapien
20	39	63.9	1411	3	Q96QW6	Q96qw6 homo sapien
21	39	63.9	1513	3	Q9HDV4	Q9hdv4 schizosacch
22	38	62.3	91	13	Q7T3K0	Q7t3k0 oncorhynchu
23	38	62.3	207	3	O09411	O09411 arthroderma
24	38	62.3	318	12	Q68691	Q68691 hepatitis c
25	38	62.3	324	5	O16608	O16608 caenorhabdi
26	38	62.3	425	10	Q8L424	Q8l424 arabidopsis
27	38	62.3	577	5	Q8I291	Q8i291 plasmodium
28	38	62.3	616	5	Q20852	Q20852 caenorhabdi
29	38	62.3	658	10	Q9FYQ8	Q9fyq8 arabidopsis
30	38	62.3	658	13	Q7ZUF5	Q7zuf5 brachydanio
31	38	62.3	662	11	Q8C7F9	Q8c7f9 mus musculu
32	38	62.3	662	11	Q8C6H4	Q8c6h4 mus musculu
33	38	62.3	1829	5	Q19815	Q19815 caenorhabdi
34	37	60.7	54	5	Q8IF84	Q8if84 trypanosoma
35	37	60.7	105	5	Q8NIN9	Q8nin9 cladosporiu
36	37	60.7	178	16	Q9L5F5	Q9l5f5 salmonella
37	37	60.7	184	10	Q9SYM6	Q9sym6 arabidopsis
38	37	60.7	191	12	Q80GI4	Q80gi4 human echov
39	37	60.7	251	12	Q9Q8N8	Q9q8n8 myxoma viru
40	37	60.7	251	12	Q9Q913	Q9q913 shope fibro
41	37	60.7	272	16	Q8DJU6	Q8dju6 synechococc
42	37	60.7	347	10	Q7XVB5	Q7xvb5 oryza sativ
43	37	60.7	377	16	Q7VBI4	Q7vbi4 prochloroco
44	37	60.7	389	3	Q872N5	Q872n5 neurospora
45	37	60.7	401	10	Q93YR2	Q93yr2 arabidopsis

ALIGNMENTS

RESULT 1
Q9GLX1

ID   Q9GLX1   PRELIMINARY;   PRT;   122 AA.
AC   Q9GLX1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor-D (Fragment).
GN   VEGF-D.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Mandriota S.J., Pepper M.S.;
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF099135; AAG29747.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 2.
DR   ProDom; PD001629; PD_growth_factor; 1.
FT   NON_TER   1   1
FT   NON_TER   122   122
SQ   SEQUENCE 122 AA; 13820 MW; CC504B00E29D54EB CRC64;

Query Match   70.5%; Score 43; DB 6; Length 122;
Best Local Similarity   100.0%; Pred. No. 3.5;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
              |||||||||
Db   1 ISVPLTSVP 9

RESULT 2
Q8QGD7
ID   Q8QGD7   PRELIMINARY;   PRT;   252 AA.
AC   Q8QGD7;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor D.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Diaz-Trelles R., Rodriguez-Leon J., Kawakami Y.,
RA   Izpisua-Belmonte J.C.;
RT   "Expression of the chick vascular endothelial growth factor D gene
RT   during limb development.";
RL   Mech. Dev. 0:0-0(2002).
DR   EMBL; AF479650; AAM12733.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   252 AA; 28767 MW; 643475DAB2E72F27 CRC64;

Query Match   70.5%; Score 43; DB 13; Length 252;
  Best Local Similarity   100.0%;
  Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
              |||||||||
Db   168 ISVPLTSVP 176

RESULT 3
Q9IZE4
ID   Q9IZE4   PRELIMINARY;   PRT;   326 AA.
AC   Q9IZE4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   VEGF-D.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,
RA   Pepper M.S., Giannis A., Sleeman J.P.;
RT   "Characterization of indolinones which specifically inhibit VEGF-C and
RT   VEGF-D-induced activation of VEGFR-3 but not VEGFR-2.";
RL   Eur. J. Biochem. 0:0-0(2001).
DR   EMBL; AY032728; AAK96008.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 1.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   326 AA; 37106 MW; D7CABBA6C9FABB7D CRC64;

Query Match   70.5%; Score 43; DB 11; Length 326;
  Best Local Similarity   100.0%;
  Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
              |||||||||
Db   173 ISVPLTSVP 181

RESULT 4
Q9GUB7
ID   Q9GUB7   PRELIMINARY;   PRT;   348 AA.
AC   Q9GUB7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   F25E5.13.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilson R., Bradshaw H.;
RT   "The sequence of C. elegans cosmid F25E5.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF078157; AAG24081.1; -.
DR   WormPep; F25E5.13; CE24915.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR   InterPro; IPR003003; 7TM_chemrecept2.
DR   InterPro; IPR000168; Nm7TM_chemrecept.
DR   Pfam; PF01604; 7tm_5; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   348 AA; 39882 MW; 456DEC8833CF3176 CRC64;

Query Match   68.9%; Score 42; DB 5; Length 348;
  Best Local Similarity   54.5%;
  Matches   6; Conservative   2; Mismatches   3; Indels   0; Gaps   0;

Qy   1 CISVPLTSVPC 11
              ||.|||||.||
Db   33 CFSIQIVSIPC 43

RESULT 5
Q8C7W1
ID   Q8C7W1   PRELIMINARY;   PRT;   118 AA.
AC   Q8C7W1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   C330008L01RIK OR AW048023.

OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK049158; BAC33576.1; -.
DR   MGD; MGI:2147036; C330008L01Rik.
KW   Hypothetical protein.
SQ   SEQUENCE   118 AA;   12658 MW;   7245EA4643F9123A CRC64;

Query Match   67.2%; Score 41; DB 11; Length 118;
Best Local Similarity 54.5%; Pred. No. 8;
Matches   6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy   1 CISVPLTSVPC 11
         |:||||| ||
Db   95 CLPTPLTPTPC 105

RESULT 6
Q9NF93
ID   Q9NF93   PRELIMINARY;   PRT;   208 AA.
AC   Q9NF93;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical transmembrane protein L8032.05a.
GN   L8032.05A.
OS   Leishmania major.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5664;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Friedlin;
RA   Ivens A.C., Murphy L., Quail M., Harris D., Oliver K., Lawson D.,
RA   Rajandream M.A., Barrell B.G.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Friedlin;
RX   MEDLINE=98146435; PubMed=9477341;
RA   Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA   Smith D.F.;
RT   "A physical map of the Leishmania major Friedlin genome.";
RL   Genome Res. 8:135-145(1998).
DR   EMBL; AL139794; CAC22646.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
KW   Transmembrane.
SQ   SEQUENCE   208 AA;   23200 MW;   11DB7F6DDDC566A3 CRC64;

Query Match   65.6%; Score 40; DB 5; Length 208;
Best Local Similarity 63.6%; Pred. No. 21;
Matches   7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy   1 CISVPLTSVPC 11
         |:||||| ||
Db   96 CVSVPLMSACC 106

RESULT 7
Q8VIA1
ID   Q8VIA1   PRELIMINARY;   PRT;   474 AA.
AC   Q8VIA1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Np95 (Fragment).
GN   NP95.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kanari Y., Kubo E., Kurihara T., Takabe T., Tatsumi K., Muto M.;
RT   "Targeted Disruption of Np95 Gene Renders ES cells Hypersensitive to
RT   DNA Damage and DNA Replication Blocks.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB066245; BAB79496.1; -.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003105; G9a.
DR   InterPro; IPR000566; Lipocln_cytFABP.
DR   InterPro; IPR000626; Ubiquitin.
DR   InterPro; IPR001965; Znf_PHD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00628; PHD; 1.
DR   Pfam; PF00240; ubiquitin; 1.
DR   Pfam; PF02182; YDG_SRA; 1.
DR   PRINTS; PR00348; UBIQUITIN.
DR   SMART; SM00249; PHD; 1.
DR   SMART; SM00213; UBQ; 1.
DR   PROSITE; PS00213; LIPOCALIN; 1.
DR   PROSITE; PS50053; UBIQUITIN_2; 1.
DR   PROSITE; PS01359; ZF_PHD_1; 1.
DR   PROSITE; PS50016; ZF_PHD_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
FT   NON_TER   474   474
SQ   SEQUENCE   474 AA;   53685 MW;   0EAE841CCD8C7FEA CRC64;

Query Match   65.6%; Score 40; DB 11; Length 474;
Best Local Similarity 70.0%; Pred. No. 46;
Matches   7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy   1 CISVPLTSVP 10
         |:|||||||
Db 349 CLKPPLTSVP 358

RESULT 8
Q8VDF2
ID   Q8VDF2   PRELIMINARY;   PRT;   782 AA.
AC   Q8VDF2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nuclear protein 95.
GN   NP95.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022167; AAH22167.1; -.
DR   MGD; MGI:1338889; Np95.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003105; G9a.
DR   InterPro; IPR000566; Lipocln_cytFABP.
DR   InterPro; IPR000626; Ubiquitin.
DR   InterPro; IPR001965; Znf_PHD.

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DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00628; PHD; 1.
DR   Pfam; PF00240; ubiquitin; 1.
DR   Pfam; PF02182; YDG_SRA; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   PRINTS; PR00348; UBIQUITIN.
DR   SMART; SM00249; PHD; 1.
DR   SMART; SM00184; RING; 2.
DR   SMART; SM00466; SRA; 1.
DR   SMART; SM00213; UBQ; 1.
DR   PROSITE; PS00213; LIPOCALIN; 1.
DR   PROSITE; PS00053; UBIQUITIN_2; 1.
DR   PROSITE; PS01359; ZF_PHD_1; 1.
DR   PROSITE; PS50016; ZF_PHD_2; 1.
DR   PROSITE; PS55016; ZF_PHD; 1.
DR   PROSITE; PS50518; ZF_RING_1; 1.
DR   PROSITE; PS50089; ZF_RING_2; 2.
SQ   SEQUENCE  782 AA;  88303 MW;  DC5EEDFCDF69619B CRC64;

Query Match             65.6%;  Score 40;  DB 11;  Length 782;
Best Local Similarity   70.0%;  Pred. No. 74;
Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CISVPLTSVP 10
                |:  ||||||
Db        349 CLKPPLTSVP 358

RESULT 10
Q9Y9B5
ID   Q9Y9B5      PRELIMINARY;      PRT;    169 AA.
AC   Q9Y9B5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein APE2372.
GN   APE2372.
OS   Aeropyrum pernix.
OC   Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC   Desulfurococcaceae; Aeropyrum.
OX   NCBI_TaxID=56636;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K1;
RX   MEDLINE=99310339; PubMed=10382966;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA   Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA   Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA   Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA   Yanazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA   Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT   "Complete genome sequence of an aerobic hyper-thermophilic
RT   crenarchaeon, Aeropyrum pernix K1.";
RL   DNA Res. 6:83-101(1999).
DR   EMBL; AP000064; BAA81385.1; -.
DR   PIR; A72466; A72466.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE  169 AA;  17432 MW;  9BDB7147C7B1426A CRC64;

Query Match             63.9%;  Score 39;  DB 17;  Length 169;
Best Local Similarity   60.0%;  Pred. No. 26;
Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CISVPLTSVP 10
                || :|:| |||
Db         57 CIGIPVASVP 66

RESULT 11
Q9PY69
ID   Q9PY69      PRELIMINARY;      PRT;    318 AA.
AC   Q9PY69;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   P1 protease (Fragment).
OS   Soybean mosaic virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC   Potyvirus.
OX   NCBI_TaxID=12222;
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RESULT 9
Q9Z1H6
ID   Q9Z1H6      PRELIMINARY;      PRT;    782 AA.
AC   Q9Z1H6;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nuclear protein np95 (Nuclear zinc finger protein Np95).
GN   NP95 OR UHRF1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pre-Tcell;
RX   MEDLINE=99099250; PubMed=9880673;
RA   Fujimori A., Matsuda Y., Takemoto Y., Hashimoto Y., Kubo E., Araki R.,
RA   Fukumura R., Mita K., Tatsumi K., Muto M.;
RT   "Cloning and mapping of Np95 gene which encodes a novel nuclear
RT   protein associated with cell proliferation.";
RL   Mamm. Genome 9:1032-1035(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Davenport J.W., Fernandes E.R., Neale G.A.M., Goorha R.M.;
RT   "LMO2-induced T cell leukemias overexpress Np95, a gene containing
RT   RING and PHD zinc fingers and an ubiquitin-like domain.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; D87908; BAA74579.1; -.
DR   EMBL; AF274046; AAK55743.1; -.
DR   HSSP; Q15843; 1NDD.
DR   MGD; MGI:1338889; Np95.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003105; G9a.
DR   InterPro; IPR000566; Lipocln_cytFABP.
DR   InterPro; IPR000626; Ubiquitin.
DR   InterPro; IPR001965; Znf_PHD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00628; PHD; 1.
DR   Pfam; PF00240; ubiquitin; 1.
DR   Pfam; PF02182; YDG_SRA; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   PRINTS; PR00348; UBIQUITIN.
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RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ch1;
RA   Latorre I.J., Domier L.L., Hartman G.L.;
RT   "Natural variability of soybean mosaic virus.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF200544; AAF13954.1; -.
DR   GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR002540; Poty_P1.
DR   Pfam; PF01577; Poty_P1; 1.
KW   Protease.
FT   NON_TER       1      1
FT   NON_TER     318    318
SQ   SEQUENCE   318 AA;  36291 MW;  0D2C1B46035AEAF1 CRC64;

Query Match             63.9%;  Score 39;  DB 12;  Length 318;
  Best Local Similarity   70.0%;  Pred. No. 48;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 ISVPLTSVPC 11
          |||:|:|:||
Db     20 ISVPNTHIPC 29


RESULT 12
Q7U7P2
ID   Q7U7P2;                 PRELIMINARY;        PRT;   366 AA.
AC   Q7U7P2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative glycerol dehydrogenase (EC 1.1.1.6).
GN   SYNW0939.
OS   Synechococcus sp. (strain WH8102).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX   NCBI_TaxID=84588;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22825697; PubMed=12917641;
RA   Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,
RA   Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
RA   Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT   "The genome of a motile marine Synechococcus.";
RL   Nature 424:1037-1042(2003).
DR   EMBL; BX569691; CAE07454.1; -.
KW   Oxidoreductase; Complete proteome.
SQ   SEQUENCE   366 AA;  38076 MW;  4C9E5230413AA11B CRC64;

Query Match             63.9%;  Score 39;  DB 16;  Length 366;
  Best Local Similarity   54.5%;  Pred. No. 55;
  Matches    6;  Conservative    3;  Mismatches    3;  Indels    2;  Gaps    0;

Qy      1 CISVPLTSVPC 11
          |||:|:|:||
Db    113 CITVPLSAATC 123


RESULT 13
Q7V6T2
ID   Q7V6T2;                 PRELIMINARY;        PRT;   386 AA.
AC   Q7V6T2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative glycerol dehydrogenase (EC 1.1.1.6).
GN   GLDA OR PMT1062.
OS   Prochlorococcus marinus (strain MIT 9313).
OC   Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC   Prochlorococcus.
OX   NCBI_TaxID=74547;
RN   [1]
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RP   SEQUENCE FROM N.A.
RX   MEDLINE=22825698; PubMed=12917642;
RA   Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
RA   Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA   Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
RA   Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA   Webb E.A., Zinser E.R., Chisholm S.W.;
RT   "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT   niche differentiation.";
RL   Nature 424:1042-1047(2003).
DR   EMBL; BX572098; CAE21237.1; -.
KW   Oxidoreductase; Complete proteome.
SQ   SEQUENCE   386 AA;  41291 MW;  2CAC614ACF010B1B CRC64;

Query Match             63.9%;  Score 39;  DB 16;  Length 386;
  Best Local Similarity   54.5%;  Pred. No. 57;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CISVPLTSVPC 11
          |||:|:|:||
Db    122 CITVPLSAATC 132


RESULT 14
Q8NA51
ID   Q8NA51;                 PRELIMINARY;        PRT;   500 AA.
AC   Q8NA51;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ35838.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA   Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA   Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA   Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA   Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA   Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA   Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK093157; BAC04077.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   Pfam; PF00041; fn3; 1.
DR   SMART; SM00060; FN3; 4.
KW   Hypothetical protein.
SQ   SEQUENCE   500 AA;  53566 MW;  0107DFF313725F40 CRC64;

Query Match             63.9%;  Score 39;  DB 4;  Length 500;
  Best Local Similarity   77.8%;  Pred. No. 74;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 SVPLTSVPC 11
          ||||:|:||
Db    303 SVPLETVPC 311


RESULT 15
Q9XGQ5
ID   Q9XGQ5;                 PRELIMINARY;        PRT;   661 AA.
AC   Q9XGQ5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   ESTs AU064813 (E40579).
OS   Oryza sativa (Rice).
```

OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC
RT   clone:P0026F07.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP000364; BAA81763.1; -.
DR   Gramene; Q9XGQ5; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR004240; EMP70.
DR   Pfam; PF02990; EMP70; 1.
SQ   SEQUENCE   661 AA; 74533 MW; 612242C132F68E8E CRC64;

Query Match   63.9%; Score 39; DB 10; Length 661;
Best Local Similarity   88.9%; Pred. No. 96;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CISVPLTSV 9
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Db   478 CISVPLTLV 486

Search completed: September 5, 2004, 09:59:56
Job time : 26.8889 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:37:49 ; Search time 36.1111 Seconds
                                             (without alignments)
                                             86.068 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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               6: geneseqp2003as:*
               7: geneseqp2003bs:*
               8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	11	4	AAU04526	Aau04526 VEGF base
2	59	96.7	11	4	AAU04542	Aau04542 VEGF base
3	57	93.4	11	4	AAU04545	Aau04545 VEGF base
4	54	88.5	11	4	AAU04543	Aau04543 VEGF base
5	52	85.2	11	4	AAU04544	Aau04544 VEGF base
6	45.5	74.6	10	4	AAU04532	Aau04532 VEGF base
7	43	70.5	96	4	AAU04520	Aau04520 Human VEG
8	43	70.5	109	3	AAY23889	Aay23889 Human vas
9	43	70.5	109	3	AAB11931	Aabl1931 Human tru
10	43	70.5	109	6	ABB84621	Abb84621 Human wil
11	43	70.5	109	6	ABG73750	Abg73750 Human VEG
12	43	70.5	110	5	AAM47933	Aam47933 Mouse VEG
13	43	70.5	178	2	AAY08287	Aay08287 Human gro
14	43	70.5	287	6	ABG73779	Abg73779 Human NVR
15	43	70.5	321	5	AAW53243	Aaw53243 Mus muscu
16	43	70.5	321	5	AAM47931	Aam47931 Mouse VEG
17	43	70.5	325	4	AAW53240	Aaw53240 Homo sapi
18	43	70.5	325	4	AAY97572	Aay97572 Human VEG
19	43	70.5	326	2	AAW44296	Aaw44296 Rat vascu
20	43	70.5	337	2	AAY08286	Aay08286 Human gro
21	43	70.5	354	2	AAW44293	Aaw44293 Human vas
22	43	70.5	354	2	AAW49036	Aaw49036 Human zve
23	43	70.5	354	4	AAW53241	Aaw53241 Homo sapi
24	43	70.5	354	3	AAB10649	Aab10649 Human VEG
25	43	70.5	354	3	AAY70750	Aay70750 Human pre
26	43	70.5	354	3	AAY70983	Aay70983 Human vas
27	43	70.5	354	3	AAB29049	Aab29049 Human VEG
28	43	70.5	354	4	AAB37606	Aab37606 Human VEG
29	43	70.5	354	4	AAB70685	Aab70685 Human vas
30	43	70.5	354	4	AAY97573	Aay97573 Human VEG
31	43	70.5	354	4	AAU08441	Aau08441 Polypepti
32	43	70.5	354	5	ABG33055	Abg33055 Human vas
33	43	70.5	354	5	ABG32046	Abg32046 Human Flt
34	43	70.5	354	6	ABB84623	Abb84623 Human VEG
35	43	70.5	354	7	ADD08950	Add08950 Human VEG
36	43	70.5	358	2	AAW14992	Aaw14992 Murine c-
37	43	70.5	358	2	AAW44295	Aaw44295 Mouse vas
38	43	70.5	358	5	AAW53242	Aaw53242 Mus muscu
39	43	70.5	358	5	AAM47930	Aam47930 Mouse VEG
40	43	70.5	620	2	AAW14994	Aawl4994 Human c-F
41	42	68.9	39	4	AAY07909	Aay07909 Human sec
42	41	67.2	9	4	AAU04533	Aau04533 VEGF base
43	41	67.2	60	4	AAU33238	Aau33238 Novel hum
44	41	67.2	121	3	AAG04076	Aag04076 Human sec
45	40	65.6	40	7	ABM74219	Abm74219 DNA clone

ALIGNMENTS

RESULT 1
AAU04526
ID   AAU04526 standard; peptide; 11 AA.
XX
AC   AAU04526;
XX
DT   26-SEP-2001 (first entry)
XX
DE   VEGF based monocyclic peptide 3.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Disulfide-bond 1..11
FT   /note= "This bond cyclises the peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Claim 49; Page 32; 102pp; English.
XX
CC   The sequence represents a monomeric monocyclic peptide of the invention,
CC   whose 3-dimensional structure is modeled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a

```
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 11 AA;

Query Match             100.0%;  Score 61;  DB 4;  Length 11;
Best Local Similarity   100.0%;  Pred. No. 0.0016;
Matches   11;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CISVPLTSVPC 11
              |||||||||||
Db          1 CISVPLTSVPC 11


RESULT 2
AAU04542
ID   AAU04542 standard; peptide; 11 AA.
XX
AC   AAU04542;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based monocyclic peptide 20.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Disulfide-bond 1..11
FT                  /note= "This bond cyclises the peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 25; Page 47; 102pp; English.
XX
CC   The sequence represents a monomeric monocyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal. The mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 11 AA;

Query Match             96.7%;  Score 59;  DB 4;  Length 11;
Best Local Similarity   90.9%;  Pred. No. 0.0034;
Matches   10;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy          1 CISVPLTSVPC 11
              |:|||||||||
Db          1 ClSVPLTSVPC 11


RESULT 3
AAU04545
ID   AAU04545 standard; peptide; 11 AA.
XX
AC   AAU04545;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based monocyclic peptide 23.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Disulfide-bond 1..11
FT                  /note= "This bond cyclises the peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
```

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PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 25; Page 47; 102pp; English.
XX
CC   The sequence represents a monomeric monocyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 11 AA;

Query Match             93.4%;  Score 57;  DB 4;  Length 11;
Best Local Similarity   81.8%;  Pred. No. 0.0072;
Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CISVPLTSVPC 11
              |:|||||:|||
Db          1 CVSVPLTTVPC 11

RESULT 4
AAU04543
ID   AAU04543 standard; peptide; 11 AA.
XX
AC   AAU04543;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based monocyclic peptide 21.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  1..11
FT                   /note= "This bond cyclises the peptide"
XX
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PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 25; Page 47; 102pp; English.
XX
CC   The sequence represents a monomeric monocyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 11 AA;

Query Match             88.5%;  Score 54;  DB 4;  Length 11;
Best Local Similarity   72.7%;  Pred. No. 0.023;
Matches    8;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CISVPLTSVPC 11
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Db          1 CITIPLTSLPC 11

RESULT 5
AAU04544
ID   AAU04544 standard; peptide; 11 AA.
XX
AC   AAU04544;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based monocyclic peptide 22.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
```

```
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key              Location/Qualifiers
FT   Disulfide-bond   1..11
FT                    /note= "This bond cyclises the peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 25; Page 47; 102pp; English.
XX
CC   The sequence represents a monomeric monocyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 11 AA;

Query Match             85.2%;  Score 52;  DB 4;  Length 11;
Best Local Similarity   72.7%;  Pred. No. 0.049;
Matches    8;  Conservative   3;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CISVPLTSVPC 11
              ||| |::|:||||
Db          1 CISLPISSVPC 11
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```
RESULT 6
AAU04532
ID   AAU04532 standard; peptide; 10 AA.
XX
AC   AAU04532;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based monocyclic peptide 10.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key              Location/Qualifiers
FT   Disulfide-bond   1..10
FT                    /note= "This bond cyclises the peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Claim 49; Page 32; 102pp; English.
XX
CC   The sequence represents a monomeric monocyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 10 AA;

Query Match             74.6%;  Score 45.5;  DB 4;  Length 10;
Best Local Similarity   90.9%;  Pred. No. 0.52;
Matches   10;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   1;
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Qy           1 CISVPLTSVPC 11
               |||||| |||
Db           1 CISVPL-SVPC 10

RESULT 7
AAU04520
ID   AAU04520 standard; protein; 96 AA.
XX
AC   AAU04520;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human VEGF-D amino acids Val101-PRO186.
XX
KW   Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG,  Hughes RA,  Stacker S,  Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 1; Page 89; 102pp; English.
XX
CC   The sequence represents Human VEGF-D (vascular endothelial growth factor)
CC   amino acids Val101-PRO186. The sequence is used in a method of producing
CC   a monomeric monocyclic peptide by a measuring beta-beta carbon separation
CC   distances on opposite antiparallel strands of a peptide loop fragment
CC   from an exposed loop of a growth factor protein and cyclising the peptide
CC   by oxidising the cysteine residues. The monocyclic peptides; dimeric
CC   bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
CC   peptide with at least one amino acid deleted prior to cyclisation are
CC   used to interfere with angiogenesis, neovascularisation or
CC   lymphangiogenesis in a mammal with a condition characterised by
CC   angiogenesis, neovascularisation or lymphangiogenesis. The condition is
CC   diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
CC   malignant or benign tumour, post-recovery cerebrovascular accident, post-
CC   angioplasty restenosis, head, heat or cold trauma, substance-induced
CC   neovascularisation of the liver, excessive hormone-related angiogenic
CC   dysfunction, diabetes induced neovascular sequelae, hypertension induced
CC   neovascular sequelae, or chronic liver infection. The peptides are also
CC   used to modulate vascular permeability in a mammal (the mammal has a
CC   condition characterised by fluid accumulation in peripheral limbs or in
CC   lungs, peritoneal cavity, pleura, or brain. The peptides are used to
CC   image blood vessels and lymphatic vasculature. The monomeric and bicyclic
CC   peptides are used to interfere with at least one biological activity
CC   induced by VEGF, VEGF-C or -D and are also used in combination with an
CC   anti-inflammatory agent, to treat a chronic inflammation, especially
CC   rheumatoid arthritis, psoriasis and diabetic retinopathy.
XX
SQ   Sequence 96 AA;
```

```
Query Match             70.5%;  Score 43;  DB 4;  Length 96;
Best Local Similarity  100.0%;  Pred. No. 14;
Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           2 ISVPLTSVP 10
               |||||||||
Db          68 ISVPLTSVP 76

RESULT 8
AAY23889
ID   AAY23889 standard; protein; 109 AA.
XX
AC   AAY23889;
XX
DT   21-SEP-1999  (first entry)
XX
DE   Human vascular endothelial growth factor (VEGF)-D.
XX
KW   Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma;
KW   tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft;
KW   wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.
XX
OS   Homo sapiens.
XX
PN   WO993348S-A1.
XX
PD   08-JUL-1999.
XX
PF   23-DEC-1998;  98WO-US027373.
XX
PR   24-DEC-1997;  97AU-00001131.
PR   29-MAY-1998;  98US-0087392P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG,  Stacker SA,  Alitalo K;
XX
DR   WPI; 1999-405368/34.
XX
PT   A human cell line stably expressing vascular endothelial growth factor D,
PT   useful for treating melanomas or tumors expressing VEGF-D.
XX
PS   Claim 6; Page 72; 79pp; English.
XX
CC   The present sequence represents human vascular endothelial growth factor
CC   (VEGF)-D. The specification describes a human cell line which stably
CC   expresses VEGF-D, or fragments/analogues having VEGF-D biological
CC   activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex
CC   DNA, VEGF-D variants or antibodies (especially chimeric antibodies), are
CC   useful for the treatment or alleviation of malignant melanomas, tumours
CC   or psoriasis. Angiogenesis and lymphangiogenesis stimulating amounts of
CC   VEGF-D can be administered to enhance the acceptance and/or healing of
CC   skin grafts or to stimulate the healing of a surgical or traumatic wound
CC   to the skin. Lymphangiogenesis stimulating amounts of VEGF-D can be used
CC   to treat lymphedema. Endothelial proliferation stimulating amounts of
CC   VEGF-D are used to treat scleroderma. Vascularisation stimulating amounts
CC   of VEGF-D can be used to treat anhydrotic ectodermal dysplasia. VEGF-D
CC   antibodies are useful for detecting tumours expressing VEGF-D. Fully-
CC   processed VEGF-D can be used to stimulate at least one VEGF-D bioactivity
CC   chosen from endothelial cell proliferation, migration, survival and
CC   differentiation and lymphangiogenesis without inducing vascular
CC   permeability
XX
SQ   Sequence 109 AA;
```

```
Query Match             70.5%;  Score 43;  DB 2;  Length 109;
Best Local Similarity  100.0%;  Pred. No. 16;
Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           2 ISVPLTSVP 10
               |||||||||
Db          76 ISVPLTSVP 84
```

RESULT 9
AAB11931
ID   AAB11931 standard; protein; 109 AA.
XX
AC   AAB11931;
XX
DT   20-NOV-2000 (first entry)
XX
DE   Human truncated VEGF-D.
XX
KW   Truncated VEGF-D; vascular endothelial growth factor; human;
KW   monoclonal antibody; VEGF receptor; VEGFR-2; VEGFR-3;
KW   vascular permeability disorder; endothelial cell proliferative disorder;
KW   angiogenic disorder; lymphangiogenic disorder;
KW   neovascularisation disorder; endothelial cell differentiation disorder;
KW   cancer; diabetic retinopathy; psoriasis; arthropathy; pulmonary oedema;
KW   detection; diagnosis; imaging; lymphatic vasculature.
XX
OS   Homo sapiens.
XX
PN   WO200037025-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US031332.
XX
PR   21-DEC-1998;   98US-0113254P.
PR   17-MAY-1999;   99US-0134556P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Stacker SA;
XX
DR   WPI; 2000-442498/38.
XX
PT   Novel compositions comprising antibodies reactive to vascular endothelial
PT   growth factor-D, useful for treating, e.g. angiogenesis, lymphogiogenesis
PT   and neovascularization disorders.
XX
PS   Claim 1; Fig 1; 44pp; English.
XX
CC   This sequence represents a 109 amino acid truncated human VEGF-D
CC   (vascular endothelial growth factor D), lacking both the N- and C-
CC   terminal regions. The invention relates to a monoclonal antibody, or
CC   fragments thereof, which is specifically reactive with the truncated
CC   human VEGF-D, and methods of preparing the antibody. The antibody of the
CC   invention interferes with the binding of VEGF-D to the VEGF receptors
CC   VEGFR-2 and VEGFR-3, but does not interfere with the binding of VEGF to
CC   these receptors and additionally is not reactive with VEGF-C. The
CC   antibody may be used to treat disorders associated with vascular
CC   permeability, endothelial cell proliferation, angiogenesis,
CC   lymphangiogenesis, neovascularisation and endothelial cell
CC   differentiation, especially cancer, diabetic retinopathy, psoriasis, and
CC   arthropathies. The antibody may also be used to treat fluid accumulation
CC   in the heart and/or lung via modulation of vascular permeability. It may
CC   additionally be used to detect VEGF-D and may be used to image lymphatic
CC   vasculature in tissue
XX
SQ   Sequence 109 AA;

Query Match   70.5%; Score 43; DB 3; Length 109;
Best Local Similarity   100.0%; Pred. No. 16;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
              |||||||||
Db   76 ISVPLTSVP 84

RESULT 10
ABB84621
ID   ABB84621 standard; protein; 109 AA.
XX
AC   ABB84621;
XX
DT   01-APR-2003 (first entry)
XX
DE   Human wild-type VEGF-D monomer SEQ ID 3.
XX
KW   Human; single-chain; extracellular ligand-binding domain; VEGF;
KW   vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
KW   VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
KW   lymphangiogenesis.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Region   8..18
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"
FT   Region   36..49
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"
FT   Region   55..60
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"
FT   Misc-difference 60
FT   /note= "This residues is described as Gln in Claim 9"
FT   Region   70..86
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"
XX
PN   WO200281520-A2.
XX
PD   17-OCT-2002.
XX
PF   08-APR-2002; 2002WO-DK000233.
XX
PR   06-APR-2001; 2001DK-00000578.
PR   06-APR-2001; 2001US-0282239P.
XX
PA   (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI   Boesen TP, Halkier T;
XX
DR   WPI; 2003-058505/05.
XX
PT   Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds
PT   to extracellular ligand-binding domain of vascular endothelial growth
PT   factor type 2/type 3 receptor but does not activate the receptor.
XX
PS   Claim 9; Page 66; 71pp; English.
XX
CC   This invention describes a novel single-chain dimeric polypeptide which
CC   binds to extracellular ligand-binding domain of vascular endothelial
CC   growth factor (VEGF) type 2 receptor (KDR) or VEGF type 3 receptor (Flt-
CC   4). The polypeptide of the invention comprises two receptor-binding sites
CC   of which one is capable of binding to a ligand-binding domain of the
CC   receptor and one is incapable of effectively binding to a ligand-binding
CC   domain of the receptor, and at least one monomer of the dimeric
CC   polypeptide is derived from VEGF, VEGF-C or VEGF-D, where the polypeptide
CC   is capable of binding to the receptor, but incapable of activating the
CC   receptor. The polypeptide of the invention is useful for preparing a
CC   medicament for preventing or treating a disease or condition involving
CC   increased signal transduction from, or an increased activation of a VEGF
CC   type 2 or type 3 receptor e.g. for inhibiting angiogenesis or
CC   lymphangiogenesis. This sequence represents a human single-chain VEGF-D
CC   monomer which can be modified and used in the construction of a VEGF-
CC   based KDR antagonist described in the disclosure of the invention
XX
SQ   Sequence 109 AA;

Query Match   70.5%; Score 43; DB 6; Length 109;
Best Local Similarity   100.0%; Pred. No. 16;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 ISVPLTSVP 10
              |||||||||
Db         76 ISVPLTSVP 84
```

RESULT 11
ABG73750
ID   ABG73750 standard; protein; 109 AA.
XX
AC   ABG73750;
XX
DT   01-APR-2003 (first entry)
XX
DE   Human VEGF-D monomer unit E57R variant.
XX
KW   Human; single-chain; extracellular ligand-binding domain; VEGF;
KW   vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
KW   VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
KW   lymphangiogenesis; mutant; mutein; variant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT
FT   Misc-difference 10
FT   /note= "This wild-type residue is replaced by Arg or Glu
FT   in the first monomer unit of the VEGF-D dimer if the E57R
FT   mutation has not occurred (see Claim 16) and is
FT   optionally replaced if the E57R mutation has occurred.
FT   The claim describes this residue as Ser but is shown as
FT   Ile in the sequence listing"
FT   Misc-difference 37
FT   /note= "This wild-type Asn residue is optionally replaced
FT   by Arg in the second monomer unit of the VEGF-D dimer
FT   (See Claim 11)"
FT   Misc-difference 38
FT   /note= "This wild type Thr residue is optionally replaced
FT   by Arg or Glu in the second monomer unit of the VEGF-D
FT   dimer (see Claims 11 and 16)"
FT   Misc-difference 39
FT   /note= "This wild type Phe residue is optionally replaced
FT   by Arg or Glu in the second monomer unit of the VEGF-D
FT   dimer (see Claims 11 and 16)"
FT   Misc-difference 40
FT   /note= "This wild type Phe residue is optionally replaced
FT   by Arg in the second monomer unit of the VEGF-D dimer
FT   (see Claim 11)"
FT   Misc-difference 57
FT   /label= E57R
FT   /note= "Wild type Gln is replaced by Arg in the first
FT   monomer unit of the VEGF-D dimer (See Claim 11) and is
FT   optionally replaced if the S10R/E mutation has occurred
FT   (see Claim 16)"
FT   Misc-difference 76
FT   /note= "This wild type Ile residue is optionally replaced
FT   by Arg or Glu in the second monomer unit of the VEGF-D
FT   dimer (see Claim 16)"
XX
PN   WO200281520-A2.
XX
PD   17-OCT-2002.
XX
PF   08-APR-2002; 2002WO-DK000233.
XX
PR   06-APR-2001; 2001DK-00000578.
PR   06-APR-2001; 2001US-0282239P.
XX
PA   (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI   Boesen TP, Halkier T;
XX

DR   WPI; 2003-058505/05.
XX
PT   Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds
PT   to extracellular ligand-binding domain of vascular endothelial growth
PT   factor type 2/type 3 receptor but does not activate the receptor.
XX
PS   Claim 11; Page; 71pp; English.
XX
CC   This invention describes a novel single-chain dimeric polypeptide which
CC   binds to extracellular ligand-binding domain of vascular endothelial
CC   growth factor (VEGF) type 2 receptor (KDR) or VEGF type 3 receptor (Flt-
CC   4). The polypeptide of the invention comprises two receptor-binding sites
CC   of which one is capable of binding to a ligand-binding domain of the
CC   receptor and one is incapable of effectively binding to a ligand-binding
CC   domain of the receptor, and at least one monomer of the dimeric
CC   polypeptide is derived from VEGF, VEGF-C or VEGF-D, where the polypeptide
CC   is capable of binding to the receptor, but incapable of activating the
CC   receptor. The polypeptide of the invention is useful for preparing a
CC   medicament for preventing or treating a disease or condition involving
CC   increased signal transduction from, or an increased activation of a VEGF
CC   type 2 or type 3 receptor e.g. for inhibiting angiogenesis or
CC   lymphangiogenesis. This sequence represents a variant of the human VEGF-D
CC   monomer unit used in the construction of a VEGF-D dimer described in the
CC   disclosure of the invention. In one instance a polypeptide is claimed
CC   comprising a first monomer derived from VEGF-D having at least the
CC   mutation E57R and optionally comprising a second monomer derived from
CC   VEGF-D having at least one mutation selected from the group consisting of
CC   N37R, T38T, F39R and F40R. In a second instance a polypeptide is claimed
CC   comprising a first monomer containing a substitution consisting of S10R,
CC   S10E and E57R (although the residue at position 10 is an Ile), and/or in
CC   the other VEGF-D derived monomer at least one substitution selected from
CC   the group consisting of T38R, T38E, F39R, F39E, I76R and I76E. NOTE: This
CC   sequence is not represented in the body of the specification but has been
CC   constructed from the wild-type VEGF-D sequence represented in ABB8621
XX
SQ   Sequence 109 AA;

Query Match   70.5%; Score 43; DB 6; Length 109;
Best Local Similarity   100.0%; Pred. No. 16;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 ISVPLTSVP 10
              |||||||||
Db         76 ISVPLTSVP 84
```

RESULT 12
AAM47933
ID   AAM47933 standard; protein; 110 AA.
XX
AC   AAM47933;
XX
DT   28-FEB-2002 (first entry)
XX
DE   Mouse VEGF-D VHD domain SEQ ID NO 6.
XX
KW   Mouse; vascular endothelial growth factor-D; VEGF-D; proliferation;
KW   lymph vessel endothelial cell; VEGF receptor-3; neoplastic disease;
KW   VEGF-PDGF homology domain; VHD.
XX
OS   Mus sp.
XX
PN   WO200182870-A2.
XX
PD   08-NOV-2001.
XX
PF   03-MAY-2001; 2001WO-US014295.
XX
PR   03-MAY-2000; 2000US-0201421P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Stacker S;

XX
DR   WPI; 2002-049310/06.
DR   N-PSDB; ABA05427.
XX
PT   Specific activating of VEGF receptor-3, useful for stimulating
PT   proliferation and/or maintaining of only lymph vessel endothelial cells,
PT   by administration of a polypeptide having high sequence identity with the
PT   mouse VEGF-D polypeptide.
XX
PS   Claim 1; Page 41; 41pp; English.
XX
CC   The invention relates to a method for activating only vascular
CC   endothelial growth factor (VEGF) receptor-3 comprising administering to a
CC   cell bearing the receptor an active amount of a composition comprising a
CC   polypeptide having at least 90%, preferably 95%, sequence identity with
CC   the mouse VEGF-D polypeptide or its fragment. The polypeptide
CC   specifically activates VEGF receptor-3 which results in proliferation of
CC   lymph vessel endothelial cells. The polypeptide is useful for activating
CC   only VEGF receptor-3 and is therefore useful for stimulating
CC   proliferation and/or maintaining of only lymph vessel endothelial cells.
CC   The polypeptide is also useful in the diagnosis of a neoplastic disease
CC   characterized by an increase in lymph vessel endothelial cells. The mouse
CC   VEGF-D has two isoforms. The longer amino acid sequence designated mVEGF-
CC   D1 (AAM47930) has an insertion of five amino acids (AAM47932) after
CC   residue 30 and diverges in the C-terminal sequence after residue 317
CC   compared to the shorter isoform mVEGF-D2, which diverges after residue
CC   312. The present sequence is that of the VEGF-PDGF homology domain (VHD),
CC   comprising residues 92-201 of the full length mouse VEGF-D2 protien of
CC   the invention
XX
SQ   Sequence 110 AA;

Query Match   70.5%;   Score 43;   DB 5;   Length 110;
Best Local Similarity 100.0%;   Pred. No. 16;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
        |||||||||
Db   77 ISVPLTSVP 85

RESULT 13
AAY08287
ID   AAY08287 standard; protein; 178 AA.
XX
AC   AAY08287;
XX
DT   14-JUL-1999 (first entry)
XX
DE   Human growth factor protein fragment FIGF178 (VEGF-D178).
XX
KW   Growth factor; human; dimer; cysteine knot; cellular inclusion body;
KW   pharmaceutical.
XX
OS   Homo sapiens.
XX
PN   DE19748734-A1.
XX
PD   06-MAY-1999.
XX
PF   05-NOV-1997; 97DE-01048734.
XX
PR   05-NOV-1997; 97DE-01048734.
XX
PA   (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX
PI   Kaerst U, Mueller C, Rinas U, Weich H, Erdmann H;
XX
DR   WPI; 1999-278785/24.
XX
PT   Preparing active growth factor dimers from inclusion bodies in high
PT   yield.
XX

PS   Claim 14; Page 9; 14pp; German.
XX
CC   This invention describes the novel preparation of biologically active
CC   dimers of recombinant human growth factors of the cysteine knot family
CC   starting from cellular inclusion bodies. Such dimers are are useful in
CC   pharmaceutical compositions and the method provides yields of 31-39.7%
CC   in examples, compared with about 10% for the conventional method (see
CC   Biochemistry, 28 (1989) 2956). AAY08278-Y08301 are human growth factor
CC   protein fragments used in the method of the invention
XX
SQ   Sequence 178 AA;

Query Match   70.5%;   Score 43;   DB 2;   Length 178;
Best Local Similarity 100.0%;   Pred. No. 27;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
        |||||||||
Db 153 ISVPLTSVP 161

RESULT 14
ABG73779
ID   ABG73779 standard; protein; 287 AA.
XX
AC   ABG73779;
XX
DT   03-APR-2003 (first entry)
XX
DE   Human NVR protein.
XX
KW   NVR; human; endothelial growth factor; cytostatic; cancer; angiogenesis;
KW   cell proliferation; revascularisation; amputation; vasculogenesis;
KW   transplant; brain; breast; intestine; kidney; lung; ovary; pancreas;
KW   prostate; uterus; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Misc-difference 281
FT   /note= "Encoded by TAA, an in frame stop codon which
FT   interrupts the coding region as shown in Figure 1A-B.
FT   This site is the end of the protein sequence represented
FT   in SEQ ID 1 of the Sequence listing"
FT   Region   282..287
FT   /note= "Region not represented in SEQ ID 1 of the
FT   Sequence listing"
XX
PN   US2002155538-A1.
XX
PD   24-OCT-2002.
XX
PF   09-JAN-2002; 2002US-00044622.
XX
PR   23-JAN-1997; 97US-00788812.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Bandman O, Goli SK, Murry LE;
XX
DR   WPI; 2003-182635/18.
DR   N-PSDB; ABQ77105.
XX
PT   New endothelial growth factor polypeptide and polynucleotides, useful for
PT   diagnosing, preventing, and treating cancer and other conditions or
PT   diseases involving angiogenesis and cell proliferation.
XX
PS   Claim 1; Fig 1A-B; 28pp; English.
XX
CC   This invention describes a novel human endothelial growth factor
CC   polypeptide which has cytostatic activity. The polypeptide and its
CC   encoding polynucleotide are useful in the diagnosis, prevention, and
CC   treatment of cancer and other conditions or diseases involving

CC   angiogenesis and cell proliferation. NVR may also be used to promote
CC   revascularisation following traumatic amputation and surgical
CC   reconstruction or added to a tissue culture to promote vasculogenesis in
CC   tissues for autologous or heterologous transplant. Antagonists or
CC   inhibitors of NVR may be used to suppress or prevent angiogenesis and
CC   thus prevent the growth and development of cancers such as cancer of the
CC   brain, breast, intestine, kidney, lung, ovary, pancreas, prostate or
CC   uterus. The products of the invention can be used for gene therapy. This
CC   sequence represents the human NVR protein described in the disclosure of
CC   the invention
XX
SQ   Sequence 287 AA;

Query Match   70.5%; Score 43; DB 6; Length 287;
Best Local Similarity   100.0%; Pred. No. 44;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
              |||||||||
Db   168 ISVPLTSVP 176

RESULT 15
AAW53243
ID   AAW53243 standard; protein; 321 AA.
XX
AC   AAW53243;
XX
DT   03-AUG-1998 (first entry)
XX
DE   Mus musculus vascular endothelial growth factor D2 (VEGF-D2).
XX
KW   vascular endothelial growth factor; VEGF-D; angiogenesis; modification;
KW   acceleration; wound healing; tissue; organ; transplants;
KW   collateral circulation; infarction; arterial stenosis;
KW   coronary artery disease; diabetic retinopathy; cancer; treatment;
KW   diabetic retinopathy; lung disorders; blood circulation;
KW   gaseous exchange; chronic obstructive airway disease;
KW   intestinal malabsorptive syndrome; biopsy; metastatic risk; detection;
KW   diagnosis; congestive heart failure.
XX
OS   Mus musculus.
XX
PN   WO9807832-A1.
XX
PD   26-FEB-1998.
XX
PF   21-AUG-1997;   97WO-US014696.
XX
PR   23-AUG-1996;   96AU-00001825.
PR   23-AUG-1996;   96US-0023751P.
PR   01-NOV-1996;   96AU-00003554.
PR   14-NOV-1996;   96US-0031099P.
PR   05-FEB-1997;   97AU-00004954.
PR   10-FEB-1997;   97US-0038814P.
PR   19-JUN-1997;   97AU-00007435.
PR   01-JUL-1997;   97US-0051426P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
PI   Achen MG, Wilks AF, Stacker SA, Alitalo K;
XX
DR   WPI; 1998-179057/16.
DR   N-PSDB; AAV20809.
XX
PT   New isolated vascular endothelial growth factor-D - used to develop
PT   products for use in e.g. modifying angiogenesis or treating lung, heart
PT   or intestinal disorders.
XX
PS   Claim 16; Page 64-65; 101pp; English.
XX
CC   The sequence is that of mouse lung vascular endothelial growth factor D2

CC   (VEGF-D2). VEGF-D2 can be used for e.g. acceleration of angiogenesis in
CC   wound healing, tissue or organ transplantation, or to establish
CC   collateral circulation in tissue infarction or arterial stenosis, such as
CC   coronary artery disease, and inhibition of angiogenesis in the treatment
CC   of cancer or of diabetic retinopathy. It can also be used in the
CC   treatment of lung disorders to improve blood circulation in the lung
CC   and/or gaseous exchange between the lungs and the blood stream or to
CC   improve blood circulation to the heart and O2 gas permeability in cases
CC   of cardiac insufficiency, to improve blood flow and gaseous exchange in
CC   chronic obstructive airway disease, or to treat malabsorptive syndromes
CC   in the intestinal tract. Quantitation of VEGF-D in cancer biopsy
CC   specimens may be useful as an indicator of future metastatic risk.
CC   Antagonists can be used for treating e.g. conditions such as congestive
CC   heart failure, involving accumulations of fluid in the lung resulting
CC   from increases in vascular permeability. The products can also be used
CC   for detection and diagnosis
XX
SQ   Sequence 321 AA;

Query Match   70.5%; Score 43; DB 2; Length 321;
Best Local Similarity   100.0%; Pred. No. 49;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
              |||||||||
Db   168 ISVPLTSVP 176

Search completed: September 5, 2004, 09:55:11
Job time : 37.1111 secs

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                    GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:     September 5, 2004, 10:00:15 ; Search time 30.8889 Seconds
                                         (without alignments)
                                         112.199 Million cell updates/sec

Title:        US-09-761-636A-7
Perfect score: 61
Sequence:     1 CISVPLTSVPC 11

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      1298764 segs, 315065143 residues

Total number of hits satisfying chosen parameters:      1298764

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	61	100.0	11	9	US-09-761-636A-7	Sequence 7, Appli
2	59	96.7	11	9	US-09-761-636A-23	Sequence 23, Appl
3	57	93.4	11	9	US-09-761-636A-26	Sequence 26, Appl
4	54	88.5	11	9	US-09-761-636A-24	Sequence 24, Appl
5	52	85.2	11	9	US-09-761-636A-25	Sequence 25, Appl
6	45.5	74.6	10	9	US-09-761-636A-13	Sequence 13, Appl
7	43		49	13	US-10-139-876-11	Sequence 11, Appl
8	43	70.5	81	13	US-10-086-623-18	Sequence 18, Appl
9	43	70.5	81	14	US-10-260-539-18	Sequence 18, Appl
10	43	70.5	96	9	US-09-761-636A-1	Sequence 1, Appli
11	43	70.5	109	9	US-09-956-095-3	Sequence 3, Appli
12	43	70.5	109	9	US-09-219-345A-1	Sequence 1, Appli
13	43	70.5	109	16	US-10-779-731-1	Sequence 1, Appli
14	43	70.5	110	10	US-09-847-524-6	Sequence 6, Appli
15	43	70.5	197	12	US-10-352-153-8	Sequence 8, Appli
16	43	70.5	280	13	US-10-044-622-1	Sequence 1, Appli
17	43	70.5	321	10	US-09-847-524-4	Sequence 4, Appli
18	43	70.5	321	14	US-10-274-953-9	Sequence 9, Appli
19	43	70.5	321	14	US-10-161-694-9	Sequence 9, Appli
20	43	70.5	325	14	US-10-274-953-3	Sequence 3, Appli
21	43	70.5	325	14	US-10-161-694-3	Sequence 3, Appli
22	43	70.5	354	9	US-09-956-095-2	Sequence 2, Appli
23	43	70.5	354	9	US-09-219-345A-11	Sequence 11, Appl
24	43	70.5	354	9	US-09-795-006A-119	Sequence 119, App
25	43	70.5	354	10	US-09-375-248-6	Sequence 6, Appli
26	43	70.5	354	12	US-09-765-534B-22	Sequence 22, Appli
27	43	70.5	354	12	US-10-661-740-6	Sequence 6, Appli
28	43	70.5	354	14	US-10-262-538-26	Sequence 26, Appl
29	43	70.5	354	14	US-10-274-953-5	Sequence 5, Appli
30	43	70.5	354	14	US-10-161-694-5	Sequence 5, Appli
31	43	70.5	354	14	US-10-174-930-1	Sequence 1, Appli
32	43	70.5	358	9	US-09-852-209A-13	Sequence 13, Appl
33	43	70.5	358	10	US-09-847-524-2	Sequence 2, Appli
34	43	70.5	358	12	US-10-439-337A-13	Sequence 13, Appl
35	43	70.5	358	12	US-10-303-997B-13	Sequence 13, Appl
36	43	70.5	358	13	US-10-139-876-2	Sequence 2, Appli
37	43	70.5	358	14	US-10-131-600-13	Sequence 13, Appl
38	43	70.5	358	14	US-10-274-953-8	Sequence 8, Appli
39	43	70.5	358	14	US-10-161-694-8	Sequence 8, Appli
40	43	70.5	362	14	US-10-139-876-4	Sequence 4, Appli
41	42	68.9	39	14	US-10-195-730-172	Sequence 172, App
42	42	68.9	39	16	US-10-799-747-172	Sequence 172, App
43	41	67.2	9	9	US-09-761-636A-14	Sequence 14, Appl
44	40	65.6	80	12	US-10-206-915-576	Sequence 576, App
45	40	65.6	80	12	US-10-199-670-576	Sequence 576, App

ALIGNMENTS

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RESULT 1
US-09-761-636A-7
; Sequence 7, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
;  APPLICANT: ACHEN, Marc
;  APPLICANT: STACKER, Steven
;  APPLICANT: HUGHES, Richard
;  APPLICANT: CENDRON, Angela
;  TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
;  FILE REFERENCE: 1064/48505 Achen et al
;  CURRENT APPLICATION NUMBER: US/09/761,636A
;  CURRENT FILING DATE: 2001-01-18
;  PRIOR APPLICATION NUMBER: US 60/176,293
;  PRIOR FILING DATE: 2000-01-18
;  PRIOR APPLICATION NUMBER: US 60/204,590
;  PRIOR FILING DATE: 2000-05-16
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.0
;
; SEQ ID NO 7
;  LENGTH: 11
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-761-636A-7

  Query Match             100.0%;  Score 61;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0036;
  Matches   11;  Conservative  0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CISVPLTSVPC 11
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Db          1 CISVPLTSVPC 11

RESULT 2
US-09-761-636A-23
; Sequence 23, Application US/09761636A
; Patent No. US20020065218A1
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GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-23

Query Match   96.7%; Score 59; DB 9; Length 11;
Best Local Similarity   90.9%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CISVPLTSVPC 11
       |:|||||||||
Db 1 CLSVPLTSVPC 11

RESULT 3
US-09-761-636A-26
; Sequence 26, Application US/09761636A1
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-26

Query Match   93.4%; Score 57; DB 9; Length 11;
Best Local Similarity   81.8%; Pred. No. 0.015;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CISVPLTSVPC 11
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Db 1 CVSVPLTTVPC 11

RESULT 4
US-09-761-636A-24
; Sequence 24, Application US/09761636A1
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela

; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-24

Query Match   88.5%; Score 54; DB 9; Length 11;
Best Local Similarity   72.7%; Pred. No. 0.046;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CISVPLTSVPC 11
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Db 1 CITIPLTSLPC 11

RESULT 5
US-09-761-636A-25
; Sequence 25, Application US2002006521BA1
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-25

Query Match   85.2%; Score 52; DB 9; Length 11;
Best Local Similarity   72.7%; Pred. No. 0.095;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CISVPLTSVPC 11
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Db 1 CISLPISSVPC 11

RESULT 6
US-09-761-636A-13
; Sequence 13, Application US/09761636A1
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293

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; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-13

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Best Local Similarity  90.9%;  Pred. No. 0.93;
Matches   10; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

Qy    1 CISVPLTSVPC 11
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Db    1 CISVPL-SVPC 10

RESULT 7
US-10-139-876-11
; Sequence 11, Application US10139876
; Publication No. US20020123481A1
; GENERAL INFORMATION:
; APPLICANT: Oliviero, Salvatore
; TITLE OF INVENTION: C-Fos Induced Growth Factor (Figf) And Dna Encoding Same
; FILE REFERENCE: 35784/205172
; CURRENT APPLICATION NUMBER: US/10/139,876
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/043,476
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: PCT/IB96/0113
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: GB9612368.2
; PRIOR FILING DATE: 1996-06-13
; PRIOR APPLICATION NUMBER: GB9519928.7
; PRIOR FILING DATE: 1995-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(48)
; OTHER INFORMATION: segment of FIGF
US-10-139-876-11

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Best Local Similarity  100.0%;  Pred. No. 11;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy    2 ISVPLTSVP 10
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Db   23 ISVPLTSVP 31

RESULT 8
US-10-086-623-18
; Sequence 18, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/086,623
; CURRENT FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: PDGF/VEGF-homology domain of VEGF-D
US-10-086-623-18

Query Match       70.5%;  Score 43; DB 13; Length 81;
Best Local Similarity  100.0%;  Pred. No. 18;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy    2 ISVPLTSVP 10
        |||||||||
Db   58 ISVPLTSVP 66

RESULT 9
US-10-260-539-18
; Sequence 18, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
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;   LENGTH: 81
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   OTHER INFORMATION: PDGF/VEGF-homology domain of VEGF-D
US-10-260-539-18

Query Match             70.5%;  Score 43;  DB 14;  Length 81;
Best Local Similarity   100.0%;  Pred. No. 18;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          2 ISVPLTSVP 10
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Db         58 ISVPLTSVP 66


RESULT 10
US-09-761-636A-1
; Sequence 1, Application US/09761636A
; Patent No. US2002006521BA1
; GENERAL INFORMATION:
;   APPLICANT: ACHEN, Marc
;   APPLICANT: STACKER, Steven
;   APPLICANT: HUGHES, Richard
;   APPLICANT: CENDRON, Angela
;   TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
;   FILE REFERENCE: 1064/48505 Achen et al
;   CURRENT APPLICATION NUMBER: US/09/761,636A
;   CURRENT FILING DATE: 2001-01-18
;   PRIOR APPLICATION NUMBER: US 60/176,293
;   PRIOR FILING DATE: 2000-01-18
;   PRIOR APPLICATION NUMBER: US 60/204,590
;   PRIOR FILING DATE: 2000-05-16
;   NUMBER OF SEQ ID NOS: 34
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 96
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   OTHER INFORMATION: Amino acid residues of Val101-Pro196 of VEGF-D
US-09-761-636A-1

Query Match             70.5%;  Score 43;  DB 9;  Length 96;
Best Local Similarity   100.0%;  Pred. No. 22;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          2 ISVPLTSVP 10
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Db         68 ISVPLTSVP 76


RESULT 11
US-09-956-095-3
; Sequence 3, Application US/09956095
; Patent No. US2002010226OA1
; GENERAL INFORMATION:
;   APPLICANT: ACHEN, Marc G.
;   APPLICANT: STACKER, Steven A.
;   TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
;   TITLE OF INVENTION:  VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
;   TITLE OF INVENTION:  FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
;   TITLE OF INVENTION:  VASCULARIZATION OF TISSUE
;   FILE REFERENCE: 1064/48666PC
;   CURRENT APPLICATION NUMBER: US/09/956,095
;   CURRENT FILING DATE: 2001-09-20
;   PRIOR APPLICATION NUMBER: 09/796,714
;   PRIOR FILING DATE: 2001-03-02
;   PRIOR APPLICATION NUMBER: 60/234,196
;   PRIOR FILING DATE: 2000-09-20
;   NUMBER OF SEQ ID NOS: 4
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;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-956-095-3

Query Match             70.5%;  Score 43;  DB 9;  Length 109;
Best Local Similarity   100.0%;  Pred. No. 24;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          2 ISVPLTSVP 10
              |||||||||
Db         76 ISVPLTSVP 84


RESULT 12
US-09-219-345A-1
; Sequence 1, Application US/09219345A
; Patent No. US2002012722A1
; GENERAL INFORMATION:
;   APPLICANT: ACHEN, Marc
;   TITLE OF INVENTION:  EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR
;   TITLE OF INVENTION:  ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING
;   TITLE OF INVENTION:  MELANOMAS
;   FILE REFERENCE:  1064/44385 Marc ACHEN
;   CURRENT APPLICATION NUMBER: US/09/219,345A
;   CURRENT FILING DATE: 1998-12-23
;   PRIOR APPLICATION NUMBER: AU PP 1131
;   PRIOR FILING DATE: 1997-12-24
;   PRIOR APPLICATION NUMBER:  US 60/087,392
;   PRIOR FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-219-345A-1

Query Match             70.5%;  Score 43;  DB 9;  Length 109;
Best Local Similarity   100.0%;  Pred. No. 24;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          2 ISVPLTSVP 10
              |||||||||
Db         76 ISVPLTSVP 84


RESULT 13
US-10-779-731-1
; Sequence 1, Application US/10779731
; Publication No. US2004014I917A1
; GENERAL INFORMATION:
;   APPLICANT: ACHEN, Marc G.
;   APPLICANT:  STACKER, Steve A.
;   TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
;   FILE REFERENCE: ACHEN et al-1064-44660
;   CURRENT APPLICATION NUMBER: US/10/779,731
;   CURRENT FILING DATE:  2004-02-18
;   PRIOR APPLICATION NUMBER: US/10/100,037
;   PRIOR FILING DATE: 2002-03-19
;   PRIOR APPLICATION NUMBER: 09/469,186
;   PRIOR FILING DATE: 1999-12-21
;   PRIOR APPLICATION NUMBER: 60/113,254
;   PRIOR FILING DATE: 1998-12-21
;   PRIOR APPLICATION NUMBER: 60/134,556
;   PRIOR FILING DATE: 1999-05-17
;   NUMBER OF SEQ ID NOS: 1
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 109
;   TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-779-731-1

Query Match   70.5%;   Score 43;   DB 16;   Length 109;
Best Local Similarity   100.0%;   Pred. No. 24;
Matches   9;   Conservative   9;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   2 ISVPLTSVP 10
            |||||||||
Db   76 ISVPLTSVP 84

RESULT 14
US-09-847-524-6
; Sequence 6, Application US/09847524
; Publication No. US2003016652 3A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G
; APPLICANT: STACKER, Steven A
; TITLE OF INVENTION: A METHOD FOR ACTIVATING ONLY THE VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR RECEPTOR-3 AND USES THEREOF
; FILE REFERENCE: Achen&Stacker-mouse VEFG-D
; CURRENT APPLICATION NUMBER: US/09/847,524
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Murinae gen. sp.
US-09-847-524-6

Query Match   70.5%;   Score 43;   DB 10;   Length 110;
Best Local Similarity   100.0%;   Pred. No. 25;
Matches   9;   Conservative   9;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   2 ISVPLTSVP 10
            |||||||||
Db   77 ISVPLTSVP 85

RESULT 15
US-10-352-153-8
; Sequence 8, Application US/10352153
; Publication No. US2003021110 1A1
; GENERAL INFORMATION:
; APPLICANT: Wise, Lyn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stacker, Stephen
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
; TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
; TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence Listing for 09/431,833
; CURRENT APPLICATION NUMBER: US/10/352,153
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US/09/431,888A
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,689
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,800
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-352-153-8

Query Match   70.5%;   Score 43;   DB 12;   Length 197;
Best Local Similarity   100.0%;   Pred. No. 44;

Matches   9;   Conservative   9;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   2 ISVPLTSVP 10
            |||||||||
Db   92 ISVPLTSVP 100

Search completed: September 5, 2004, 10:29:18
Job time : 30.8889 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:55:30 ; Search time 9.77778 Seconds
                                        (without alignments)
                                        58.079 Million cell updates/sec

Title: US-09-761-636a-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents AA:*
                1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
                2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
                3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
                4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
                5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	70.5	109	4	US-09-469-186-1	Sequence 1, Appli
2	43	70.5	109	4	US-09-469-185-1	Sequence 1, Appli
3	43	70.5	197	4	US-09-431-888-8	Sequence 8, Appli
4	43	70.5	321	3	US-08-915-795-9	Sequence 9, Appli
5	43	70.5	325	3	US-08-915-795-5	Sequence 5, Appli
6	43	70.5	354	3	US-08-915-795-5	Sequence 5, Appli
7	43	70.5	358	3	US-08-915-795-8	Sequence 8, Appli
8	40	65.6	79	4	US-09-134-000C-4906	Sequence 4906, Ap
9	38	62.3	663	3	US-08-959-004-5	Sequence 5, Appli
10	37	60.7	600	4	US-09-328-352-7636	Sequence 7636, Ap
11	37	60.7	1248	4	US-10-042-810-2	Sequence 2, Appli
12	37	60.7	1278	4	US-10-042-810-4	Sequence 4, Appli
13	36	59.0	388	3	US-08-861-774E-94	Sequence 94, Appl
14	36	59.0	409	4	US-09-252-991A-17910	Sequence 17910, A
15	36	59.0	533	4	US-09-508-370A-6	Sequence 6, Appli
16	36	59.0	534	4	US-09-508-370A-5	Sequence 5, Appli
17	35	57.4	90	6	522013-24	Patent No. 5220013
18	35	57.4	147	4	US-09-252-991A-23997	Sequence 23997, A
19	35	57.4	150	4	US-09-252-991A-29818	Sequence 29818, A
20	35	57.4	193	4	US-08-635-886C-227	Sequence 227, App
21	35	57.4	193	4	US-08-974-690C-227	Sequence 227, App
22	35	57.4	207	4	US-08-134-231C-22	Sequence 22, Appl
23	35	57.4	207	4	US-08-728-160-22	Sequence 22, Appl
24	35	57.4	208	3	US-08-612-973-32	Sequence 32, Appl
25	35	57.4	208	3	US-08-927-597-32	Sequence 32, Appl
26	35	57.4	299	2	US-08-923-856-1	Sequence 1, Appli
27	35	57.4	299	3	US-09-216-294-1	Sequence 1, Appli
28	35	57.4	319	4	US-08-635-886C-202	Sequence 202, App
29	35	57.4	319	4	US-08-635-886C-226	Sequence 226, App
30	35	57.4	319	4	US-08-974-690C-202	Sequence 202, App
31	35	57.4	319	4	US-08-974-690C-226	Sequence 226, App
32	35	57.4	363	1	US-08-484-105-20	Sequence 20, Appl
33	35	57.4	363	4	US-08-484-106-20	Sequence 20, Appl
34	34	55.7	1342	4	US-09-561-709B-13	Sequence 13, Appl
35	34	55.7	22	4	US-09-227-357-517	Sequence 517, App
36	34	55.7	38	1	US-08-176-500-111	Sequence 111, App
37	34	55.7	38	1	US-08-471-052A-111	Sequence 111, App
38	34	55.7	38	1	US-08-189-331-111	Sequence 111, App
39	34	55.7	38	2	US-08-471-939-111	Sequence 111, App
40	34	55.7	38	2	US-08-471-800-111	Sequence 111, App
41	34	55.7	38	2	US-08-471-068-111	Sequence 111, App
42	34	55.7	72	3	US-08-722-719-58	Sequence 58, Appl
43	34	55.7	72	4	US-09-334-951-58	Sequence 58, Appl
44	34	55.7	72	4	US-09-334-923A-58	Sequence 58, Appl
45	34	55.7	72	4	US-09-334-954A-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-09-469-186-1
; Sequence 1, Application US/09469186
; Patent No. 6383484
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,186
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-186-1

Query Match   70.5%; Score 43; DB 4; Length 109;
Best Local Similarity   100.0%; Pred. No. 5.8;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
              |||||||||
Db   76 ISVPLTSVP 84

RESULT 2
US-09-469-185-1
; Sequence 1, Application US/09469185
; Patent No. 6531185
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,185
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-469-185-1

Query Match   70.5%; Score 43; DB 4; Length 109;
Best Local Similarity   100.0%; Pred. No. 5.8;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
             |||||||||
Db   76 ISVPLTSVP 84

RESULT 3
US-09-431-888-8
; Sequence 8, Application US/09431888A
; Patent No. 6541008
; GENERAL INFORMATION:
;   APPLICANT: Wise, Lyn M
;   APPLICANT: Mercer, Andrew A
;   APPLICANT: Savory, Loreen J
;   APPLICANT: Fleming, Stephen B
;   APPLICANT: Stacker, Stephen
;   TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
;   TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
;   TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
;   FILE REFERENCE: Sequence Listing for 09/431,833
; Patent No. 6541008
;   CURRENT APPLICATION NUMBER: US/09/431,888A
;   CURRENT FILING DATE: 1999-11-02
;   EARLIER APPLICATION NUMBER: 60/106,689
;   EARLIER FILING DATE: 1998-11-02
;   EARLIER APPLICATION NUMBER: 60/106,800
;   EARLIER FILING DATE: 1998-11-03
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-431-888-8

Query Match   70.5%; Score 43; DB 4; Length 197;
Best Local Similarity   100.0%; Pred. No. 11;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
             |||||||||
Db   92 ISVPLTSVP 100

RESULT 4
US-08-915-795-9
; Sequence 9, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
;   APPLICANT: Marc G. ACHEN
;   APPLICANT: Andrew F. WILKS
;   APPLICANT: Steven A. STACKER
;   APPLICANT: Kari ALITALO
;   TITLE OF INVENTION: GROWTH FACTOR
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;   STREET: 1200 G Street, NW, Suite 700
;   CITY: Washington
;   STATE: DC
;   COUNTRY: United States of America
;   ZIP: 20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible

;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/915,795
;   FILING DATE:
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: EVANS, Joseph D.
;   REGISTRATION NUMBER: 26,269
;   REFERENCE/DOCKET NUMBER: 1064/42983
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 628-8800
;   TELEFAX: (202) 628-8844
;   TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 321 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   ORIGINAL SOURCE:
;   TISSUE TYPE: Mouse Lung
US-08-915-795-9

Query Match   70.5%; Score 43; DB 3; Length 321;
Best Local Similarity   100.0%; Pred. No. 18;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
             |||||||||
Db   168 ISVPLTSVP 176

RESULT 5
US-08-915-795-3
; Sequence 3, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
;   APPLICANT: Marc G. ACHEN
;   APPLICANT: Andrew F. WILKS
;   APPLICANT: Steven A. STACKER
;   APPLICANT: Kari ALITALO
;   TITLE OF INVENTION: GROWTH FACTOR
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;   STREET: 1200 G Street, NW, Suite 700
;   CITY: Washington
;   STATE: DC
;   COUNTRY: United States of America
;   ZIP: 20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/915,795
;   FILING DATE:
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: EVANS, Joseph D.
;   REGISTRATION NUMBER: 26,269
;   REFERENCE/DOCKET NUMBER: 1064/42983
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 628-8800
;   TELEFAX: (202) 628-8844
;   TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 325 amino acids
;   TYPE: amino acid

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        STRANDEDNESS: single
;       TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: NO
;       ORIGINAL SOURCE:
;       TISSUE TYPE: Human Breast
; US-08-915-795-3

Query Match             70.5%;  Score 43;  DB 3;  Length 325;
Best Local Similarity  100.0%;  Pred. No. 18;
Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     2  ISVPLTSVP 10
          |||||||||
Db   139  ISVPLTSVP 147

RESULT 6
US-08-915-795-5
; Sequence 5, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
;     APPLICANT: Marc G. ACHEN
;     APPLICANT: Andrew F. WILKS
;     APPLICANT: Steven A. STACKER
;     APPLICANT: Kari ALITALO
;     TITLE OF INVENTION: GROWTH FACTOR
;     NUMBER OF SEQUENCES: 11
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;       STREET: 1200 G Street, NW, Suite 700
;       CITY: Washington
;       STATE: DC
;       COUNTRY: United States of America
;       ZIP: 20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/915,795
;       FILING DATE:
;       CLASSIFICATION: 536
;     ATTORNEY/AGENT INFORMATION:
;       NAME: EVANS, Joseph D.
;       REGISTRATION NUMBER: 26,269
;       REFERENCE/DOCKET NUMBER: 1064/42983
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (202) 628-8800
;       TELEFAX: (202) 628-8844
;       TELEX: N/A
; INFORMATION FOR SEQ ID NO:    5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 354 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     HYPOTHETICAL: NO
;     ORIGINAL SOURCE:
;     TISSUE TYPE: Human Lung
; US-08-915-795-5

Query Match             70.5%;  Score 43;  DB 3;  Length 354;
Best Local Similarity  100.0%;  Pred. No. 20;
Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     2  ISVPLTSVP 10
          |||||||||
Db   168  ISVPLTSVP 176


RESULT 7
US-08-915-795-8
; Sequence 8, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
;     APPLICANT: Marc G. ACHEN
;     APPLICANT: Andrew F. WILKS
;     APPLICANT: Steven A. STACKER
;     APPLICANT: Kari ALITALO
;     TITLE OF INVENTION: GROWTH FACTOR
;     NUMBER OF SEQUENCES: 11
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;       STREET: 1200 G Street, NW, Suite 700
;       CITY: Washington
;       STATE: DC
;       COUNTRY: United States of America
;       ZIP: 20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/915,795
;       FILING DATE:
;       CLASSIFICATION: 536
;     ATTORNEY/AGENT INFORMATION:
;       NAME: EVANS, Joseph D.
;       REGISTRATION NUMBER: 26,269
;       REFERENCE/DOCKET NUMBER: 1064/42983
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (202) 628-8800
;       TELEFAX: (202) 628-8844
;       TELEX: N/A
; INFORMATION FOR SEQ ID NO:    8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 358 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     ORIGINAL SOURCE:
;     TISSUE TYPE: Mouse Lung
; US-08-915-795-8

Query Match             70.5%;  Score 43;  DB 3;  Length 358;
Best Local Similarity  100.0%;  Pred. No. 20;
Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     2  ISVPLTSVP 10
          |||||||||
Db   173  ISVPLTSVP 181

RESULT 8
US-09-134-000C-4906
; Sequence 4906, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;     APPLICANT: Lynn Doucette-Stamm et al
;     TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;     TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;     FILE REFERENCE: 032796-032
;     CURRENT APPLICATION NUMBER: US/09/134,000C
;     CURRENT FILING DATE: 1998-08-13
;     PRIOR APPLICATION NUMBER: US 60/055,778
;     PRIOR FILING DATE: 1997-08-15
;     NUMBER OF SEQ ID NOS: 6812
;     SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4906
;     LENGTH: 79
;     TYPE: PRT
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;       ORGANISM: Enterococcus faecalis
;   FEATURE:
;       NAME/KEY: MISC_FEATURE
;       LOCATION: (10)..(15)
;       OTHER INFORMATION: Amino acids 10 & 15 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-4906

Query Match             65.6%;  Score 40; DB 4; Length 79;
Best Local Similarity   70.0%;  Pred. No. 12;
Matches    7; Conservative    2; Mismatches    1; Indels    0; Gaps    0;

Qy         1 CISVPLTSVP 10
             ||:||||:|
Db        66 CITVPLTAKP 75

RESULT 9
US-08-959-004-5
; Sequence 5, Application US/08959004
; Patent No. 6197543
; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Yue, Henry
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Lal, Preeti
;   APPLICANT: Shah, Purvi
;   APPLICANT: Kaser, Matthew
;   TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE
;   TITLE OF INVENTION: PROTEINS
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Incyte Pharmaceuticals, Inc.
;       STREET: 3174 Porter Drive
;       CITY: Palo Alto
;       STATE: CA
;       COUNTRY: USA
;       ZIP: 94304
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette
;       COMPUTER: IBM Compatible
;       OPERATING SYSTEM: DOS
;       SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/959,004
;       FILING DATE: Herewith
;       CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Billings, Lucy J.
;       REGISTRATION NUMBER: 36,749
;       REFERENCE/DOCKET NUMBER: PF-0414 US
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 650-855-0555
;       TELEFAX: 650-845-4166
;       TELEX:
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 663 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;       LIBRARY: ADRETUT06
;       CLONE: 2822412
US-08-959-004-5

Query Match             62.3%;  Score 38; DB 3; Length 663;
Best Local Similarity   77.8%;  Pred. No. 2.4e+02;
Matches    7; Conservative    1; Mismatches    1; Indels    0; Gaps    0;

Qy         1 CISVPLTSV 9
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Db       479 CISVPLTFI 487
             ||||||||:

RESULT 10
US-09-328-352-7636
; Sequence 7636, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;   APPLICANT: Gary L. Breton et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;   TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: GTC99-03PA
;   CURRENT APPLICATION NUMBER: US/09/328,352
;   CURRENT FILING DATE: 1999-06-04
;   NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7636
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-7636

Query Match             60.7%;  Score 37; DB 4; Length 600;
Best Local Similarity   60.0%;  Pred. No. 3.1e+02;
Matches    6; Conservative    3; Mismatches    1; Indels    0; Gaps    0;

Qy         2 ISVPLTSVPC 11
             :|::|||||
Db        19 LSLAITSVPC 28

RESULT 11
US-10-042-810-2
; Sequence 2, Application US/10042810
; Patent No. 6570003
; GENERAL INFORMATION:
;   APPLICANT: Hu, Yi
;   APPLICANT: Burnett, Michael
;   APPLICANT: Zambrowicz, Brian
;   TITLE OF INVENTION: No. 6570003el Human 7TM Proteins and Polynucleotides Encoding th
;   FILE REFERENCE: LEX-0297-USA
;   CURRENT APPLICATION NUMBER: US/10/042,810
;   CURRENT FILING DATE: 2002-01-09
;   PRIOR APPLICATION NUMBER: US 60/261,624
;   PRIOR FILING DATE: 2001-01-09
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1248
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-042-810-2

Query Match             60.7%;  Score 37; DB 4; Length 1248;
Best Local Similarity   60.0%;  Pred. No. 6.6e+02;
Matches    6; Conservative    1; Mismatches    3; Indels    0; Gaps    0;

Qy         1 CISVPLTSVP 10
             |:.|.||||
Db       320 CLQYPFTSVP 329

RESULT 12
US-10-042-810-4
; Sequence 4, Application US/10042810
; Patent No. 6570003
; GENERAL INFORMATION:
;   APPLICANT: Hu, Yi
;   APPLICANT: Burnett, Michael
;   APPLICANT: Zambrowicz, Brian
;   TITLE OF INVENTION: No. 6570003el Human 7TM Proteins and Polynucleotides Encoding th
;   FILE REFERENCE: LEX-0297-USA
;   CURRENT APPLICATION NUMBER: US/10/042,810
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; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,624
; PRIOR FILING DATE: 2001-01-09
; SOFTWARE: FastSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 4
; LENGTH: 1278
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-042-810-4

Query Match   60.7%; Score 37; DB 4; Length 1278;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches   6; Conservative   1; Mismatches   3; Indels   0; Gaps   0;

Qy   1 CISVPLTSVP 10
          |: |||||
Db   320 CLQYPFTSVP 329

RESULT 13
US-08-861-774E-94
; Sequence 94, Application US/08861774E
; Patent No. 6297007
; GENERAL INFORMATION:
;   APPLICANT: Waters, Barbara
;   APPLICANT: Miao, Vivian
;   APPLICANT: Ho, Yap
;   APPLICANT: Tong, Seow
;   TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
;   TITLE OF INVENTION: BIOACTIVE MOLECULES
;   FILE REFERENCE: 9993-006
;   CURRENT APPLICATION NUMBER: US/08/861,774E
;   CURRENT FILING DATE: 1997-05-22
;   NUMBER OF SEQ ID NOS: 94
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
;   LENGTH: 388
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Clone ps3
US-08-861-774E-94

Query Match   59.0%; Score 36; DB 3; Length 388;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   2 ISVPLTSVP 10
          : |||||||
Db   318 VYVPLTSVP 326

RESULT 14
US-09-252-991A-17910
; Sequence 17910, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17910
;   LENGTH: 409
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-17910

Query Match   59.0%; Score 36; DB 4; Length 409;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches   6; Conservative   1; Mismatches   3; Indels   0; Gaps   0;

Qy   2 ISVPLTSVPC 11
          :| | |||
Db   42 VSAPCTVPC 51

RESULT 15
US-09-508-370A-6
; Sequence 6, Application US/09508370A
; Patent No. 6492131
; GENERAL INFORMATION:
;   APPLICANT: Dieter Soll
;   APPLICANT: Michael Ibba
;   TITLE OF INVENTION: Class I-type Lysyl-tRNA Synthetase
;   FILE REFERENCE: OCR-896
;   CURRENT APPLICATION NUMBER: US/09/508,370A
;   CURRENT FILING DATE: 2000-03-10
;   PRIOR APPLICATION NUMBER: PCT/US98/18968
;   PRIOR FILING DATE: 1998-09-09
;   NUMBER OF SEQ ID NOS: 16
;   SOFTWARE: MS Dos
; SEQ ID NO 6
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Methanococcus maripaludis
;   FEATURE:
;   NAME/KEY: lysyl t-RNA synthetase
;   OTHER INFORMATION: construct expressed in Example 1
US-09-508-370A-6

Query Match   59.0%; Score 36; DB 4; Length 533;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches   5; Conservative   3; Mismatches   2; Indels   0; Gaps   0;

Qy   2 ISVPLTSVPC 11
          |:|||::||
Db   84 IGMPlSEIPC 93

Search completed: September 5, 2004, 10:21:57
Job time : 10.7778 secs

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                Copyright  GenCore version 5.1.6
                Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   September  5, 2004, 09:47:29 ; Search time 13.0505 Seconds
                                         (without alignments)
                                         125.302 Million cell updates/sec

Title:          US-09-761-636A-8
Perfect score:  100
Sequence:       1 CASELGKSTNTFCKPPC 17

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:       283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      PIR_78:*
                1:  Pir1:*
                2:  Pir2:*
                3:  Pir3:*
                4:  Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	58	58.0	419	2	S69207	vascular endotheli
2	48	48.0	211	1	XUBSMM	methylphosphotries
3	48	48.0	330	2	T25169	hypothetical prote
4	45	45.0	371	2	B96614	hypothetical prote
5	44	44.0	1717	1	A45558	epidermal growth f
6	43	43.0	100	2	D71882	hypothetical prote
7	43	43.0	104	2	A39035	ribonuclease-relat
8	43	43.0	693	2	S64904	probable membrane
9	42	42.0	1428	2	T08852	lustrin A - Califo
10	41	41.0	223	2	B38346	ultra-high-sulfur
11	41	41.0	230	2	A38346	ultra-high-sulfur
12	41	41.0	319	2	A84947	lytB protein [impo
13	41	41.0	335	2	B45511	chitinase (EC 3.2.
14	41	41.0	397	2	AC1574	acetate kinase hom
15	41	41.0	397	2	AH1220	acetate kinase hom
16	41	41.0	406	2	T30748	hypothetical prote
17	41	41.0	439	2	S33293	testican - human
18	41	41.0	476	2	F88968	protein T27B7.2 [i
19	41	41.0	570	2	T37314	probable kexin (EC
20	41	41.0	585	2	C69336	probable electron
21	41	41.0	642	1	QQBEB5	UL77 protein - hum
22	41	41.0	669	2	S65551	factor H - bovine
23	41	41.0	815	2	T05555	DNA polymerase III
24	41	41.0	942	2	D87803	protein bli-4D lim
25	41	41.0	988	1	S35362	protein kinase C (
26	41	41.0	1174	2	T43051	protein kinase C (
27	41	41.0	1294	2	S77690	probable membrane
28	40	40.0	77	2	E97808	hypothetical prote
29	40	40.0	126	2	S30858	hypothetical prote
30	40	40.0	224	2	H70717	hypothetical prote
31	40	40.0	352	1	XYEBOT	methylated-DNA-[pr
32	40	40.0	353	2	AG0789	methylated-DNA-[pr
33	40	40.0	383	2	T17722	hypothetical prote
34	40	40.0	399	2	G96556	hypothetical prote
35	40	40.0	452	2	G82390	ada regulatory pro
36	40	40.0	472	2	G81325	Glu-tRNAGln amidot
37	40	40.0	526	2	A43567	J-kappa recombinat
38	40	40.0	550	2	A41585	J-kappa recombinat
39	40	40.0	575	2	A47214	Jk-recombination s
40	40	40.0	594	2	A42770	Suppressor of Hair
41	40	40.0	596	2	F84589	probable protein k
42	40	40.0	649	2	T33741	DNA-binding protei
43	40	40.0	833	1	S20387	outer membrane pro
44	40	40.0	833	2	T14703	F1 capsule anchori
45	40	40.0	1057	2	T15720	hypothetical prote

ALIGNMENTS

```
RESULT 1
S69207
vascular endothelial growth factor C precursor - human
N;Alternate names: FLT4 ligand DHM
C;Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence revision 01-Nov-1996 #text_change 08-Oct-1999
C;Accession: S69207; S61795; S71443; S69208; G02659
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela,
EMBO J. 15, 1751, 1996
A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand fo
A;Reference number: S69207; MUID:96203094; PMID:8612600
A;Accession: S69207
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-419 <JOU>
A;Cross-references: EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PIDN:e221096; PID:g18200
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A;Note: only a part of the translation is shown
A;Note: this is a revision to the sequence from reference S61795
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela,
EMBO J. 15, 290-298, 1996
A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (V
A;Reference number: S61795; MUID:96178224; PMID:8617204
A;Accession: S61795
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 70-419 <JOU1>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
A;Molecule type: protein
A;Residues: 'X', 104-120 <JOU2>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and sp
A;Reference number: S69208
A;Accession: S69208
A;Molecule type: mRNA
A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAB85214.1; NID:g1150988; PIDN:AAB85214.1; PID:g1150989
R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
A;Accession: G02659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-419 <MOR>
A;Cross-references: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427
C;Genetics:
A;Gene: GDB:VEGFC; VRP
A;Cross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;13-102/Domain: propeptide #status predicted <PRO>
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F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>

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Query Match         58.0%;  Score 58;  DB 2;  Length 419;
Best Local Similarity   71.4%;  Pred. No. 0.23;
  Matches  10;  Conservative   1;  Mismatches   3;  Indels   0;  Gaps   0;

Qy     4 ELGKSTNTFCKPPC 17
         | |::||||| ||||
Db   143 EFGVATNTFFKPPC 156
```

RESULT 2
XUBSMM
methylphosphotriester-DNA alkyltransferase (EC 2.1.1.-) / adaAB operon transcription act
C;Species: Bacillus subtilis
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 16-Jun-2000
C;Accession: S11483; F69582
R;Morohoshi, F.; Hayashi, K.; Munakata, N.
Nucleic Acids Res. 18, 5473-5480, 1990
A;Title: Bacillus subtilis ada operon encodes two DNA alkyltransferases.
A;Reference number: S11483; MUID:91016831; PMID:2120677
A;Accession: S11483
A;Molecule type: DNA
A;Residues: 1-211 <MOR>
A;Cross-references: EMBL:X53399; NID:g39786; PIDN:CAA37475.1; PID:g39787
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berten
  C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
  A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
  Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
  iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
  Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
  A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauuel,
  Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
  Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
  A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
  akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
  T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
  A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69582
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-211 <KUN>
A;Cross-references: GB:Z99104; GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB11974.1; PI
A;Experimental source: strain 168
C;Genetics:
A;Gene: adaA
C;Superfamily: methylphosphotriester-DNA methyltransferase; methylphosphotriester-DNA me
C;Keywords: DNA binding; DNA repair; methyltransferase; transcription regulation
F;23-207/Domain: methylphosphotriester-DNA methyltransferase homology <MPT>

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Query Match         48.0%;  Score 48;  DB 1;  Length 211;
Best Local Similarity   72.7%;  Pred. No. 4.5;
  Matches   8;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy     7 KSTNTFCKPPC 17
         ||||| ||
Db    48 KSTGIFCKPSC 58
```

RESULT 3
T25169
hypothetical protein T23F1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T25169
C;Genetics:
A;Gene: adaA
A;Wilkinson, J.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19990
A;Accession: T25169
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-330 <WIL>
A;Cross-references: EMBL:Z81129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:T23F1.6
A;Experimental source: clone T23F1
C;Genetics:
A;Gene: CESP:T23F1.6
A;Map position: 5
A;Introns: 16/3
C;Superfamily: gliadin

```
Query Match         48.0%;  Score 48;  DB 2;  Length 330;
Best Local Similarity   41.2%;  Pred. No. 6.6;
  Matches   7;  Conservative   4;  Mismatches   4;  Indels   6;  Gaps   0;

Qy     1 CASELGKSTNTFCKPPC 17
         |:: :|||| ||:|||
Db    80 CSQQCQSNTNTQCQPTC 96
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RESULT 4
B96614
hypothetical protein T15M6.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: B96614
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
  Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
  ansen, N.F.; Hughes, B.; Huizar, L.
  Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C
  C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
  Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
  ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96614
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-371 <STO>
A;Cross-references: GB:AE005173; NID:g11067306; PIDN:AAG28833.1; GSPDB:GN00141
C;Genetics:
A;Gene: T15M6.10
A;Map position: 1
C;Superfamily: Arabidopsis thaliana hypothetical protein F24M12.210

```
Query Match         45.0%;  Score 45;  DB 2;  Length 371;
Best Local Similarity   50.0%;  Pred. No. 21;
  Matches   8;  Conservative   2;  Mismatches   2;  Indels   6;  Gaps   0;

Qy     2 ASELGKSTNTFCKPPC 17
         :|||| ||
Db   224 SKEIEKSRKTFCVLPC 239
```

RESULT 5
A45558
epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Schistosoma mansoni
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A45558; S27836
R;Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
  Mol. Biochem. Parasitol. 53, 17-32, 1992
A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of e
A;Reference number: A45558; MUID:92365727; PMID:1501637
A;Accession: A45558
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1717 <SHO>
A;Cross-references: EMBL:M86396; NID:g160957; PIDN:AAA29866.1; PID:g160958
A;Note: sequence extracted from NCBI backbone (NCBIP:111129)
C;Genetics:

A;Gene: SER
C;Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F;1018-1323/Domain: protein kinase homology <KIN>
F;1026-1034/Region: protein kinase ATP-binding motif

Query Match
Best Local Similarity 44.0%;   Score 44;   DB 1;   Length 1717;
                  61.5%;   Pred. No. 1.2e+02;
Matches   8;   Conservative   2;   Mismatches   3;   Indels   0;   Gaps   0;

Qy   4 ELGKSTNTFCKPP 16
        |.:||||||
Db 1311 ELMRTFNTFCKPP 1323

RESULT 6
D71882
hypothetical protein jhp0825 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 29-Sep-1999
C;Accession: D71882
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71882
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <ARN>
A;Cross-references: GB:AE001512; GB:AE001439; NID:g4155392; PIDN:AAD06402.1; PID:g415539
C;Genetics:
A;Gene: jhp0825
C;Superfamily: conserved hypothetical protein HI0711

Query Match
Best Local Similarity 43.0%;   Score 43;   DB 2;   Length 100;
                  58.3%;   Pred. No. 14;
Matches   7;   Conservative   1;   Mismatches   4;   Indels   0;   Gaps   0;

Qy   5 LGKSTNTFCKPP 16
       ||| |||||
Db 82 LGSHSELFCKPP 93

RESULT 7
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A;Reference number: A39035; MUID:9109313l; PMID:1985896
A;Accession: A39035
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-104 <ARD>
C;Superfamily: pancreatic ribonuclease

Query Match
Best Local Similarity 43.0%;   Score 43;   DB 2;   Length 104;
                  61.5%;   Pred. No. 14;
Matches   8;   Conservative   1;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   1 CASELGKSTNTFC 13
       |.:||||||||||
Db 75 CKYKLKKSTNKFC 87

RESULT 8
S64904
probable membrane protein YLR072w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L2321
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002
C;Accession: S64904
R;Pohl, T.M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64899
A;Accession: S64904
A;Molecule type: DNA
A;Residues: 1-693 <POH>
A;Cross-references: EMBL:Z73244; NID:g1360427; PID:e245792; PID:g1360428; GSPDB:GN00012;
C;Genetics:
A;Gene: MIPS:YLR072w
A;Cross-references: SGD:S0004062
A;Map position: 12R
C;Keywords: transmembrane protein
F;634-650/Domain: transmembrane #status predicted <TMM>

Query Match
Best Local Similarity 43.0%;   Score 43;   DB 2;   Length 693;
                  50.0%;   Pred. No. 75;
Matches   7;   Conservative   3;   Mismatches   4;   Indels   0;   Gaps   0;

Qy   2 ASELGKSTNTFCKP 15
       ||| |||||||
Db 358 SSSLGSSTYYCRP 371

RESULT 9
T08852
lustrin A - California red abalone
C;Species: Haliotis rufescens (California red abalone)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T08852
R;Shen, X.; Belcher, A.M.; Hansma, P.K.; Stucky, G.D.; Morse, D.E.
J. Biol. Chem. 272, 32472-32481, 1997
A;Title: Molecular cloning and characterization of lustrin A, a matrix protein from shel
A;Reference number: Z16496; MUID:98070424; PMID:9405458
A;Accession: T08852
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1428 <SHE>
A;Cross-references: EMBL:AF023459; NID:g2723361; PIDN:AAB95154.1; PID:g2723362
A;Experimental source: tissue type mantle (shell and pearl nacre); cell type pallial
C;Superfamily: antileukoproteinase repeat homology
C;Keywords: extracellular matrix; extracellular protein
F;1382-1426/Domain: antileukoproteinase repeat homology <ALP>

Query Match
Best Local Similarity 42.0%;   Score 42;   DB 2;   Length 1428;
                  43.8%;   Pred. No. 2e+02;
Matches   7;   Conservative   3;   Mismatches   6;   Indels   0;   Gaps   0;

Qy   1 CASELGKSTNTFCKPP 16
       |.:|| |||||||
Db 1334 CRTNLQCPSNTYCKSP 1349

RESULT 10
B38346
ultra-high-sulfur keratin 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
C;Accession: A38346; B38346
R;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 266, 4024, 1991
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin d
A;Reference number: A38660; MUID:91154184; PMID:1840598
A;Accession: A38660
A;Molecule type: DNA
A;Residues: 1-223 <WO2>

A;Cross-references: GB:M37760; NID:g200963; PIDN:AAA40107.1; PID:g200964
A;Note: this is a correction
R;Wood, L.; Mills, M.J; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 265, 21375-21380, 1990
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin d
A;Reference number: B38346
A;Accession: B38346
A;Molecule type: DNA
<WOO>
A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962
A;Note: the sequence reported in this paper has been corrected. See A38660
C;Superfamily: ultra-high-sulfur keratin

Query Match   41.0%;   Score 41;   DB 2;   Length 223;
Best Local Similarity   41.2%;   Pred. No. 57;
Matches   7;   Conservative   2;   Mismatches   8;   Indels   0;   Gaps   0;

Qy   1 CASELGKSTNTFCKPPC 17
          :: |||| ||||
Db   10 CGSSCGGCGGSSCCKPVC 26

RESULT 11
A38346
ultra-high-sulfur keratin 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999
R;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 265, 21375-21380, 1990
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin d
A;Reference number: A38346; MUID:91065960; PMID:2250030
A;Accession: A38346
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-230 <WOO>
A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962
C;Superfamily: ultra-high-sulfur keratin

Query Match   41.0%;   Score 41;   DB 2;   Length 230;
Best Local Similarity   41.2%;   Pred. No. 59;
Matches   7;   Conservative   2;   Mismatches   8;   Indels   0;   Gaps   0;

Qy   1 CASELGKSTNTFCKPPC 17
          :: |||| ||||
Db   31 CGSNCGGCGGSSCCKPVC 47

RESULT 12
A84947
lytB protein [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: A84947
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: A84947
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: lytB; BU147
C;Superfamily: penicillin tolerance protein

Query Match   41.0%;   Score 41;   DB 2;   Length 319;
Best Local Similarity   66.7%;   Pred. No. 78;
Matches   8;   Conservative   1;   Mismatches   1;   Indels   3;   Gaps   0;

Qy   3 SELGKSTNTFCK 14
          :|||| ||| ||
Db   232 AELGKETGTFTK 243

RESULT 13
B45511
chitinase (EC 3.2.1.14) precursor, basic - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 22-Jun-1999
C;Accession: B45511
R;Samac, D.A.; Hironaka, C.M.; Yallaly, P.E.; Shah, D.M.
Plant Physiol. 93, 907-914, 1990
A;Title: Isolation and characterization of the genes encoding basic and acidic chitinase
A;Reference number: A45511
A;Accession: B45511
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-335 <SAM>
A;Cross-references: GB:M38240; NID:g166665; PIDN:AAA32769.1; PID:g166666
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;34-76/Domain: hevein chitin-binding domain homology <HCB>
F;89-327/Domain: plant chitinase homology <PCH>

Query Match   41.0%;   Score 41;   DB 2;   Length 335;
Best Local Similarity   50.0%;   Pred. No. 81;
Matches   9;   Conservative   1;   Mismatches   6;   Indels   2;   Gaps   1;

Qy   1 CASELGKSTNT--FCKPP 16
          | :|| :||:|
Db   50 CCSEFGWCGNTBPYCKQP 67

RESULT 14
AC1574
acetate kinase homolog AckA2 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AC1574
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1574
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96363.1; PID:g16413591; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: AckA2
C;Superfamily: acetate kinase

Query Match   41.0%;   Score 41;   DB 2;   Length 397;
Best Local Similarity   72.7%;   Pred. No. 94;
Matches   8;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

Qy   1 CASELGKSTNT 11
          || ||| |||
Db   214 CAIEAGKSVNT 224

RESULT 15
AH1220
acetate kinase homolog AckA2 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AH1220

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1220
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99246.1; PID:g16410584; GSPDB:GN00177
C;Genetics:
A;Experimental source: strain EGD-e
A;Gene: AckA2
C;Superfamily: acetate kinase

Query Match   41.0%; Score 41; DB 2; Length 397;
Best Local Similarity   72.7%; Pred. No. 94;
Matches   8; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   1 CASELGKSTNT 11
           |||| ||||||
Db   214 CAIEAGKSVNT 224

Search completed: September 5, 2004, 10:01:18
Job time : 14.0505 secs

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          GenCore version 5.1.6

          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   September 5, 2004, 09:38:39 ; Search time 7.72727 Seconds
                                 (without alignments)
                                 114.554 Million cell updates/sec

Title:        US-09-761-636A-8
Perfect score: 100
Sequence:     1 CASELGKSTNTFCKPPC 17

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:      141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :      SwissProt_42:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	80	80.0	354	1	VEGD_HUMAN	O43915 homo sapien
2	77	77.0	326	1	VEGD_RAT	O35251 rattus norv
3	77	77.0	358	1	VEGD_MOUSE	P97946 mus musculu
4	59	59.0	415	1	VEGC_MOUSE	P97953 mus musculu
5	58	58.0	419	1	VEGC_HUMAN	P49767 homo sapien
6	48	48.0	211	1	ADAA_BACSU	P19219 bacillus su
7	46	46.0	905	1	YD83_HUMAN	Q9P2G4 homo sapien
8	46	46.0	1112	1	SEN6_HUMAN	Q9ZrI homo sapien
9	45	45.0	442	1	TIC1_MOUSE	Q62288 mus musculu
10	43	43.0	104	1	RN30_RANPI	P22069 rana pipien
11	43	43.0	273	1	EX22_ARATH	Q9f180 arabidopsis
12	43	43.0	279	1	EX26_ARATH	Q9f178 arabidopsis
13	41	41.0	319	1	ISPH_BUCAI	P57247 buchnera ap
14	41	41.0	322	1	CHIT_ARATH	P19171 arabidopsis
15	41	41.0	397	1	ACK2_LISIN	Q92cn9 listeria in
16	41	41.0	397	1	ACK2_LISMO	Q8y7v1 listeria mo
17	41	41.0	439	1	TIC1_HUMAN	Q08629 homo sapien
18	41	41.0	596	1	GLMN_MOUSE	Q8bzm1 mus musculu
19	41	41.0	642	1	UL77_HCMVA	P16726 human cytom
20	41	41.0	685	1	CFAH_BOVIN	Q28085 bos taurus
21	41	41.0	943	1	BLI4_CAEEL	P51159 caenorhabdi
22	41	41.0	988	1	PCK1_SCHPO	P36582 schizosacch
23	41	41.0	1174	1	KPC1_COCHE	O42632 cochliobolu
24	41	41.0	1294	1	YOH5_YEAST	Q08234 saccharomyc
25	40.5	40.5	604	1	PGH2_CAVPO	P70682 cavia porce
26	40	40.0	224	1	LPRP_MYCTU	P71548 mycobacteri
27	40	40.0	328	1	CHIT_PHAVU	P06215 phaseolus v
28	40	40.0	353	1	ADA_SALTY	P26189 salmonella
29	40	40.0	472	1	GATB_CAMJE	Q9pn98 campylobact
30	40	40.0	475	1	GATB_CHLTE	Q8kae8 chlorobium
31	40	40.0	500	1	SUH_HUMAN	Q06330 homo sapien
32	40	40.0	501	1	SUH_XENLA	Q91880 xenopus lae
33	40	40.0	515	1	SUHL_MOUSE	O08674 mus musculu
34	40	40.0	516	1	SUHL_HUMAN	Q9ubg7 homo sapien
35	40	40.0	526	1	SUH_MOUSE	P31266 mus musculu
36	40	40.0	554	1	SUH_CIOIN	O76808 ciona intes
37	40	40.0	594	1	SUH_DROME	P28159 drosophila
38	40	40.0	833	1	CAFA_YERPE	P26949 yersinia pe
39	39	39.0	85	1	IBB3_PHAVU	P81484 phaseolus v
40	39	39.0	85	1	IBB4_PHAVU	P81483 phaseolus v
41	39	39.0	139	1	ULC8_HCMVA	P16837 human cytom
42	39	39.0	313	1	ISPH_BUCAP	Q8k9z4 buchnera ap
43	39	39.0	322	1	CHI2_BRANA	Q09023 brassica na
44	39	39.0	354	1	ADA_ECOLI	P06134 escherichia
45	39	39.0	451	1	YNV5_CAEEL	P34568 caenorhabdi

ALIGNMENTS

```
RESULT 1
VEGD_HUMAN
ID   VEGD_HUMAN     STANDARD;      PRT;    354 AA.
AC   O43915;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF).
GN   FIGF OR VEGFD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=97349118; PubMed=9205122;
RA   Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=98140120; PubMed=9479493;
RA   Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA   Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT   "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT   between the PIGA and the GRPR genes.";
RL   Genomics 47:207-216(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=98118549; PubMed=9435229;
RA   Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,
RA   Alitalo K., Stacker S.A.;
RT   "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT   tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).";
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [5]
RP   PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
RX   MEDLINE=2001413; PubMed=10542248;
RA   Stacker S.A., Stenvers K.L., Caesar C., Vitali A., Domagala T.,
RA   Nice E.C., Roufail S., Simpson R.J., Moritz R., Karpanen T.,
RA   Alitalo K., Achen M.G.;
RT   "Biosynthesis of vascular endothelial growth factor-D involves
RT   proteolytic processing which generates non-covalent homodimers.";
RL   J. Biol. Chem. 274:32127-32136(1999).
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC       and endothelial cell growth, stimulating their proliferation and
CC       migration and also has effects on the permeability of blood
CC       vessels. May function in the formation of the venous and lymphatic
CC       vascular systems during embryogenesis, and also in the maintenance
CC       of differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in lung, heart, small
CC       intestine and fetal lung, and at lower levels in skeletal muscle,
CC       colon, and pancreas.
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC       linked by disulfide bonds before secretion. The fully processed
CC       VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC       bound by non-covalent interactions.
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; D89630; BAA24264.1; -.
DR   EMBL; Y12863; CAA73370.1; -.
DR   EMBL; Y12864; CAA73371.1; -.
DR   EMBL; Y12865; CAA73371.1; JOINED.
DR   EMBL; Y12866; CAA73371.1; JOINED.
DR   EMBL; Y12867; CAA73371.1; JOINED.
DR   EMBL; Y12868; CAA73371.1; JOINED.
DR   EMBL; Y12869; CAA73371.1; JOINED.
DR   EMBL; Y12870; CAA73371.1; JOINED.
DR   EMBL; AJ000185; CAA03942.1; -.
DR   EMBL; BC027948; AAH27948.1; -.
DR   HSSP; P15692; 1VPP.
DR   Genew; HGNC:3708; FIGF.
DR   MIM; 300091; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005161; F:platelet-derived growth factor receptor bin. . .; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   InterPro; IPR000072; PD_growth_factor.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   Pfam; PF03128; CXCXC; 3.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Multigene family.
FT   SIGNAL        1     21       POTENTIAL.
```

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FT   PROPEP       22     88       OR 99 (IN A MINOR FORM).
FT   CHAIN        89    205       VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP      206    354
FT   DOMAIN      222    318       4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT                                X(1,3)-C.
FT   REPEAT      222    237       1 (APPROXIMATE).
FT   REPEAT      258    273       2.
FT   REPEAT      277    293       3.
FT   REPEAT      301    318       4.
FT   DISULFID    111    153       BY SIMILARITY.
FT   DISULFID    142    189       BY SIMILARITY.
FT   DISULFID    146    191       BY SIMILARITY.
FT   DISULFID    136    136       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    145    145       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    155    155       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    185    185       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    287    287       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   354 AA;  40404 MW;  2048D769D735173E CRC64;

Query Match             80.0%;  Score 80;  DB 1;  Length 354;
Best Local Similarity   93.8%;  Pred. No. 5.9e-06;
Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ASELGKSTNTFCKPPC 17
              ||||||||| ||||||
Db        121 ASELGKSTNTFFKPPC 136


RESULT 2
VEGD_RAT
ID   VEGD_RAT       STANDARD;      PRT;    326 AA.
AC   O35251;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF).
GN   FIGF OR VEGFD.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Yanada Y., Hirata Y., Nezu J., Shimane M.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC       and endothelial cell growth, stimulating their proliferation and
CC       migration and also has effects on the permeability of blood
CC       vessels. May function in the formation of the venous and lymphatic
CC       vascular systems during embryogenesis, and also in the maintenance
CC       of differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-3 (Flt4) receptor (By similarity).
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC       linked by disulfide bonds before secretion. The fully processed
CC       VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC       bound by non-covalent interactions (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF014827; AAB66557.1; -.
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DR   HSSP; P15692; 1VPP.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 1.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL        1     21       POTENTIAL.
FT   PROPEP       22     93       POTENTIAL.
FT   CHAIN        94    210       VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP      211    326       POTENTIAL.
FT   DOMAIN      227    317       4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT                                X(1,3)-C.
FT   REPEAT      227    242       1 (APPROXIMATE).
FT   REPEAT      263    278       2.
FT   REPEAT      282    298       3.
FT   REPEAT      306    317       4 (INCOMPLETE).
FT   DISULFID    116    158       BY SIMILARITY.
FT   DISULFID    147    194       BY SIMILARITY.
FT   DISULFID    151    196       BY SIMILARITY.
FT   DISULFID    141    141       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    150    150       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    160    160       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    190    190       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    292    292       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   326 AA;  37112 MW;  1261AFA373596C00 CRC64;

Query Match             77.0%;  Score 77;  DB 1;  Length 326;
Best Local Similarity   87.5%;  Pred. No. 1.7e-05;
Matches   14;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy         2 ASELGKSTNTFCKPPC 17
             ||||||:|||  ||||
Db       126 ASELGKTTNTFFKPPC 141

RESULT 3
VEGD_MOUSE
ID   VEGD_MOUSE   STANDARD;    PRT;   358 AA.
AC   P97946;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF).
GN   FIGF OR VEGFD.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57B1/6J; TISSUE=Fibroblast;
RX   MEDLINE=97030254; PubMed=8876195;
RA   Orlandini M., Marconcini L., Ferruzzi R., Oliviero S.;
RT   "Identification of a c-fos-induced gene that is related to the
RT   platelet-derived growth factor/vascular endothelial growth factor
RT   family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=97349118; PubMed=9205122;
RA   Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
RN   [3]
RP   DEVELOPMENTAL STAGE.
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RX   MEDLINE=98288130; PubMed=9622638;
RA   Avantaggiato V., Orlandini M., Acampora D., Oliviero S., Simeone A.;
RT   "Embryonic expression pattern of the murine figf gene, a growth factor
RT   belonging to platelet-derived growth factor/vascular endothelial
RT   growth factor family.";
RL   Mech. Dev. 73:221-224(1998).
RN   [4]
RP   RECEPTOR SPECIFICITY.
RX   MEDLINE=21276411; PubMed=11279005;
RA   Baldwin M.E., Catimel B., Nice E.C., Roufail S., Hall N.E.,
RA   Stenvers K.L., Karkkainen M.J., Alitalo K., Stacker S.A., Achen M.G.;
RT   "The specificity of receptor binding by vascular endothelial growth
RT   factor-d is different in mouse and man.";
RL   J. Biol. Chem. 276:19166-19171(2001).
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC       and endothelial cell growth, stimulating their proliferation and
CC       migration and also has effects on the permeability of blood
CC       vessels. May function in the formation of the venous and lymphatic
CC       vascular systems during embryogenesis, and also in the maintenance
CC       of differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-3 (Flt4) receptor.
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in fetal and adult lung.
CC   -!- DEVELOPMENTAL STAGE: Expressed in a dynamic pattern in several
CC       body structures and organs of the embryo such as limb buds,
CC       acoustic ganglion, teeth, heart, anterior pituitary as well as
CC       lung and kidney mesenchyme, liver, derma, and periosteum of the
CC       vertebral column.
CC   -!- INDUCTION: By the transcription factor c-fos.
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC       linked by disulfide bonds before secretion. The fully processed
CC       VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC       bound by non-covalent interactions. (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
```

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DR   EMBL; X99572; CAA67892.1; -.
DR   EMBL; D89628; BAA14002.1; -.
DR   HSSP; P15692; 1VPP.
DR   PMMA-2DPAGE; P97946; -.
DR   MGD; MGI:108037; Figf.
DR   GO; GO:0005576; C:extracellular; IDA.
DR   GO; GO:0008083; F:growth factor activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0008283; P:cell proliferation; IDA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 2.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL        1     21       POTENTIAL.
FT   PROPEP       22     93       POTENTIAL.
FT   CHAIN        94    210       VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP      211    358       POTENTIAL.
FT   DOMAIN      227    323       4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT                                X(1,3)-C.
FT   REPEAT      227    242       1 (APPROXIMATE).
FT   REPEAT      263    278       2.
```

```
FT   REPEAT         282    298       3.
FT   REPEAT         306    323       4.
FT   DISULFID       116    158       BY SIMILARITY.
FT   DISULFID       147    194       BY SIMILARITY.
FT   DISULFID       151    196       BY SIMILARITY.
FT   DISULFID       141    141       INTERCHAIN (BY SIMILARITY).
FT   DISULFID       150    150       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD       160    160       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD       190    190       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD       292    292       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE       358 AA;  40908 MW;  6636B17PBF07037C CRC64;

Query Match             77.0%;  Score 77;  DB 1;  Length 358;
Best Local Similarity   87.5%;  Pred. No. 1.9e-05;
Matches    14;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2  ASELGKSTNTFCKPPC  17
               ||||| :||||| |||
Db        126  ASELGKTNTFFKPPC  141
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RESULT 4
VEGC_MOUSE

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ID   VEGC_MOUSE     STANDARD;      PRT;   415 AA.
AC   P97953;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   01-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor C precursor (VEGF-C) (Vascular
DE   endothelial growth factor related protein) (VRP) (Flt4 ligand) (Flt4-
DE   L).
GN   VEGFC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=97164697; PubMed=9012504;
RA   Kukk E., Lymboussaki A., Taira S., Kaipainen A., Jeltsch M.,
RA   Joukov V., Alitalo K.;
RT   "VEGF-C receptor binding and pattern of expression with VEGFR-3
RT   suggests a role in lymphatic vascular development.";
RL   Development 122:3829-3837(1996).
RN   [2]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 108-126.
RC   STRAIN=BALB/c;
RX   MEDLINE=97388482; PubMed=9247316;
RA   Fitz L.J., Morris J.C., Towler P., Long A., Burgess P., Greco R.,
RA   Wang J., Gassaway R., Nickbarg E., Kovacic S., Ciarletta A.,
RA   Giannotti J., Finnerty H., Zollner R., Beier D.R., Leak L.V.,
RA   Turner K.J., Wood C.R.;
RT   "Characterization of murine Flt4 ligand/VEGF-C.";
RL   Oncogene 15:613-618(1997).
CC   -!- FUNCTION: Growth factor active in angiogenesis, and endothelial
CC       cell growth, stimulating their proliferation and migration and
CC       also has effects on the permeability of blood vessels. May
CC       function in angiogenesis of the venous and lymphatic vascular
CC       systems during embryogenesis, and also in the maintenance of
CC       differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expression detected in mesenchymal cells of
CC       postimplantation embryos, particularly in the regions where the
CC       lymphatic vessels undergo sprouting from embryonic veins, such as
CC       the perimetanephric, axillary and jugular regions, and in the
CC       developing mesenterium. Expressed in adult heart, brain, spleen,
CC       lung, liver, skeletal muscle and kidney.
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3, but only the fully processed form could activate VEGFR-2.
CC       VEGF-C first form an antiparallel homodimer linked by disulfide
CC       bonds. Before secretion, a cleavage occurs between arg-227 and
CC       ser-228 producing an heterotetramer. The next extracellular step
CC       of the processing removes the N-terminal propeptide. Finally the
CC       mature VEGF-C is composed mostly of two VEGF homology domains
CC       (VHDs) bound by non-covalent interactions (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
DR   EMBL; U73620; AAC52984.1; -.
DR   EMBL; U58112; AAB46707.1; -.
DR   HSSP; P15692; IVPP.
DR   MGD; MGI:109124; Vegfc.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 5.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL           1     31       POTENTIAL.
FT   PROPEP          32    107       BY SIMILARITY.
FT   CHAIN          108    223       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT   PROPEP         224    415       POTENTIAL.
FT   DOMAIN         276    358       4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT                                   X(1,3)-C.
FT   REPEAT         276    291       1.
FT   REPEAT         300    315       2.
FT   REPEAT         324    339       3.
FT   REPEAT         343    358       4.
FT   DISULFID       127    169       BY SIMILARITY.
FT   DISULFID       158    205       BY SIMILARITY.
FT   DISULFID       162    207       BY SIMILARITY.
FT   DISULFID       152    152       INTERCHAIN (BY SIMILARITY).
FT   DISULFID       161    161       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD       171    171       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD       201    201       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD       236    236       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE       415 AA;  46471 MW;  D9D3DD3CECC659D6 CRC64;

Query Match             59.0%;  Score 59;  DB 1;  Length 415;
Best Local Similarity   71.4%;  Pred. No. 0.023;
Matches    10;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4  ELGKSTNTFCKPPC  17
               | :|||||| |||
Db        139  EFGAATNTFFKPPC  152
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RESULT 5
VEGC_HUMAN

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ID   VEGC_HUMAN     STANDARD;      PRT;   419 AA.
AC   P49767;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Vascular endothelial growth factor C precursor (VEGF-C) (Vascular
DE   endothelial growth factor related protein) (VRP) (Flt4 ligand) (Flt4-
DE   L).
GN   VEGFC.
OS   Homo sapiens (Human).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.
RX   MEDLINE=96178224; PubMed=8617204;
RA   Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA   Saksela O., Kalkkinen N., Alitalo K.;
RT   "A novel vascular endothelial growth factor, VEGF-C, is a ligand for
RT   the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.";
RL   EMBO J. 15:290-298(1996).
RN   [2]
RP   ERRATUM.
RX   MEDLINE=96203094; PubMed=8612600;
RA   Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA   Saksela O., Kalkkinen N., Alitalo K.;
RL   EMBO J. 15:1751-1751(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glial tumor;
RX   MEDLINE=96312526; PubMed=8700872;
RA   Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.;
RT   "Vascular endothelial growth factor-related protein: a ligand and
RT   specific activator of the tyrosine kinase receptor Flt4.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97388482; PubMed=9247316;
RA   Fitz L.J., Morris J.C., Towler P., Long A., Burgess P., Greco R.,
RA   Wang J., Gassaway R., Nickbarg E., Kovacic S., Ciarletta A.,
RA   Giannotti J., Finnery H., Zolner R., Beier D.R., Leak L.V.,
RA   Turner K.J., Wood C.R.;
RT   "Characterization of murine Flt4 ligand/VEGF-C.";
RL   Oncogene 15:613-618(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 32-41, 112-121 AND 228-233, AND MUTAGENESIS OF ARG-227.
RX   MEDLINE=97377029; PubMed=9233800;
RA   Joukov V., Sorsa T., Kumar V., Jeltsch M., Claesson-Welsh L., Cao Y.,
RA   Saksela O., Kalkkinen N., Alitalo K.;
RT   "Proteolytic processing regulates receptor specificity and activity of
RT   VEGF-C.";
RL   EMBO J. 16:3898-3911(1997).
CC   -!- FUNCTION: Growth factor active in angiogenesis, and endothelial
CC       cell growth, stimulating their proliferation and migration and
CC       also has effects on the permeability of blood vessels. May
CC       function in angiogenesis of the venous and lymphatic vascular
CC       systems during embryogenesis, and also in the maintenance of
CC       differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Spleen, lymph node, thymus, appendix, bone
CC       marrow, heart, placenta, ovary, skeletal muscle, prostate, testis,
CC       colon and small intestine and fetal liver, lung and kidney, but
CC       not in peripheral blood lymphocyte.
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3, but only the fully processed form could activate VEGFR-2.
CC       VEGF-C first form an antiparallel homodimer linked by disulfide
CC       bonds. Before secretion, a cleavage occurs between arg-227 and
CC       ser-228 producing an heterotetramer. The next extracellular step
CC       of the processing removes the N-terminal propeptide. Finally the
CC       mature VEGF-C is composed mostly of two VEGF homology domains
CC       (VHDs) bound by non-covalent interactions.
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X94216; CAA63907.1; -.
DR   EMBL; U43142; AAA85214.1; -.
DR   EMBL; U58111; AAB02909.1; -.
DR   EMBL; BC035212; AAH35212.1; -.
DR   PIR; S69207; S69207.
DR   HSSP; P15692; 1VPF.
DR   Genew; HGNC:12682; VEGFC.
DR   MIM; 601528; -.
DR   GO; GO:0007515; P:lymph gland development; TAS.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   GO; GO:0006929; P:substrate-bound cell migration; TAS.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 5.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS00278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL        1     31
FT   PROPEP       32    111       OR 102.
FT   CHAIN       112    227       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT   PROPEP      228    419
FT   DOMAIN      280    362       4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT                               X(1,3)-C.
FT   REPEAT      280    295       1.
FT   REPEAT      304    319       2.
FT   REPEAT      328    343       3.
FT   REPEAT      347    362       4.
FT   DISULFID    131    173       BY SIMILARITY.
FT   DISULFID    162    209       BY SIMILARITY.
FT   DISULFID    166    211       BY SIMILARITY.
FT   DISULFID    156    156       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    165    165       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    175    175       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    205    205       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    240    240       N-LINKED (GLCNAC...) (POTENTIAL).
FT   MUTAGEN     227    227       R->S: NO PROTEOLYTIC PROCESSING AND LOWER
FT                               EFFECT ON VEGFR-2 AND VEGFR-3.
SQ   SEQUENCE   419 AA;  46883 MW;  9F598719DB3E014F CRC64;

Query Match             58.0%;  Score 58;  DB 1;  Length 419;
Best Local Similarity   71.4%;  Pred. No. 0.034;
```

Matches   10;   Conservative   1;   Mismatches   3;   Indels   0;   Gaps   0;

Qy   4 ELGKSTNTFCKPPC 17
            | | :|||| |||
Db   143 EFGVATNTFFKPPC 156

RESULT 6
ADAA_BACSU
ID   ADAA_BACSU   STANDARD;   PRT;   211 AA.
AC   P19219;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Methylphosphotriester-DNA alkyltransferase.
GN   ADAA OR BSU01810.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=91016831; PubMed=2120677;
RA   Morohoshi F., Hayashi K., Munakata N.;
RT   "Bacillus subtilis ada operon encodes two DNA alkyltransferases.";
RL   Nucleic Acids Res. 18:5473-5480(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RA   Haga K., Liu H., Yasumoto K., Takahashi H., Yoshikawa H.;
RT   "Sequence analysis of the 70kb region between 17 and 23 degree of the
RT   Bacillus subtilis chromosome.";
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA   Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA   Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA   Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA   Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA   Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA   Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA   Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA   Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA   Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA   Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA   Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA   Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA   Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA   Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA   Viari A., Wambutt R., Wedler E., Wedler H., Weitenegger T.,
RA   Winters P., Wipat A., Yamamoto H., Yamane H., Yasumoto K., Yata K.,
RA   Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
RN   [4]
RP   MUTAGENESIS.
RX   MEDLINE=92078089; PubMed=1744039;
RA   Morohoshi F., Hayashi K., Munakata N.;
RT   "Molecular analysis of Bacillus subtilis ada mutants deficient in the
RT   adaptive response to simple alkylating agents.";
RL   J. Bacteriol. 173:7834-7840(1991).
RL   -!- FUNCTION: METHYLPHOSPHOTRIESTER-DNA ALKYLTRANSFERASE IS ONE OF
CC   -!- FUNCTION: METHYLPHOSPHOTRIESTER-DNA ALKYLTRANSFERASE IS ONE OF
CC   TWO GENES REQUIRED FOR THE ADAPTIVE RESPONSE OF BACTERIA TO
CC   ALKYLATING AGENTS. IT ACCEPTS A METHYL GROUP FROM METHYLPHOSPHO-
CC   TRIESTERS AND THEN ACTS AS A TRANSCRIPTIONAL ACTIVATOR OF THE
CC   ADA OPERON.
CC   -!- COFACTOR: One zinc ion per subunit (By similarity).
CC   -!- SIMILARITY:TO THE N-TERMINAL REGION OF E.COLI ADA PROTEIN AND
CC   THE C-TERMINAL REGION OF THE ARAC/XYLS FAMILY.
CC   --
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CC   --
DR   EMBL; X53399; CAA37475.1; -.
DR   EMBL; AB006424; BAA33074.1; -.
DR   EMBL; Z99104; CAB11957.1; -.
DR   PIR; S11483; XUBSMM.
DR   HSSP; P06134; 1ADN.
DR   SubtiList; BG10166; adaA.
DR   InterPro; IPR004026; Ada_Zn_bind.
DR   InterPro; IPR000005; HTHAraC.
DR   Pfam; PF02805; Ada_Zn_binding; 1.
DR   Pfam; PF00165; HTH_AraC; 2.
DR   PRINTS; PR00032; HTHARAC.
DR   SMART; SM00342; HTH_ARAC; 1.
DR   PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR   PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW   DNA repair; Transcription regulation; Transferase; Methyltransferase;
KW   Activator; DNA-binding; Metal-binding; Zinc; Complete proteome.
FT   METAL   54   54   ZINC (BY SIMILARITY).
FT   METAL   58   58   ZINC (BY SIMILARITY).
FT   METAL   85   85   ZINC (BY SIMILARITY).
FT   METAL   88   88   ZINC (BY SIMILARITY).
FT   DNA_BIND   118   137   H-T-H MOTIF (BY SIMILARITY).
FT   ACT_SITE   85   85   ACCEPTOR FOR METHYL FROM PHOSPHOTRIESTER.
FT   MUTAGEN   86   87   KR->NC: LOSS OF ACTIVITY.
SQ   SEQUENCE   211 AA; 24299 MW; 92091082527EC27 CRC64;

Query Match   48.0%; Score 48; DB 1; Length 211;
Best Local Similarity   72.7%; Pred. No. 0.82;
Matches   8; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   7 KSTNTFCKPPC 17
             ||| |||||
Db   48 KSTGIFCKPSC 58

RESULT 7
YD83_HUMAN
ID   YD83_HUMAN   STANDARD;   PRT;   905 AA.
AC   Q9P2G4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hypothetical protein KIAA1383.
GN   KIAA1383.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20181126; PubMed=10718198;
RA   Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XVI.
RT   The complete sequences of 150 new cDNA clones from brain which code

```
RT   for large proteins in vitro.";
RL   DNA Res. 7:65-73(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Coville G.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; AB037804; BAA92621.1; ALT_INIT.
DR   EMBL; AL451083; CAC36345.1; -.
DR   EMBL; BC036663; AAH36663.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   905 AA;  100344 MW;  B02FBD0EDAD78491 CRC64;

Query Match             46.0%;  Score 46;  DB 1;  Length 905;
Best Local Similarity   57.1%;  Pred. No. 7.6;
Matches    8;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy     3  SELGKSTNTFCKPP  16
          :|| ||| |||
Db   290  TELDMETNIFCPPP  303

RESULT 8
SEN6_HUMAN
ID   SEN6_HUMAN     STANDARD;      PRT;  1112 AA.
AC   Q9GZR1; O94891; Q8TBY4; Q9UJV5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Sentrin-specific protease 6 (EC 3.4.22.-) (Sentrin/SUMO-specific
DE   protease SENP6) (SUMO-1 specific protease 1) (Protease FKSG6).
GN   SENP6 OR SSP1 OR SUSP1 OR KIAA0797.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), VARIANT CYS-1106, AND
RP   CHARACTERIZATION.
RC   TISSUE=Brain;
RX   MEDLINE=20261527; PubMed=10799485;
RA   Kim K.I., Baek S.H., Jeon Y.-J., Nishimori S., Suzuki T., Uchida S.,
RA   Shimbara N., Saitoh H., Tanaka K., Chung C.H.;
RT   "A new SUMO-1-specific protease, SUSP1, that is highly expressed in
RT   reproductive organs.";
RL   J. Biol. Chem. 275:14102-14106(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RA   Gong L., Yeh E.T.H.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Wang Y.-G.;
RT   "Identification of FKSG6, a novel protein with protease activity.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SEQUENCE OF 1-692 FROM N.A. (ISOFORM 2).
RC   TISSUE=Tongue;
RA   Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA   Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA   Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA   Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA   Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA   Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA   Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA   Isogai T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE OF 29-1112 FROM N.A. (ISOFORM 1), AND VARIANT CYS-1106.
RC   TISSUE=Brain;
RX   MEDLINE=99087487; PubMed=9872452;
RA   Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
RA   Tanaka A., Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XI.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 5:277-286(1998).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT CYS-1106.
RC   TISSUE=Brain;
RA   Ohara O., Suyama M., Nagase T., Ishikawa K., Kikuno R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Protease that releases SUMO-1 from its precursor
CC       sequence.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Name=1;
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CC       IsoId=Q9GZR1-1; Sequence=Displayed;
CC       Name=2;
CC       IsoId=Q9GZR1-2; Sequence=VSP_005274;
CC       Note=No experimental confirmation available;
CC   -!- TISSUE SPECIFICITY: Highly expressed in reproductive organs, such
CC       as testis, ovary and prostate.
CC   -!- SIMILARITY: Belongs to peptidase family C48.
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CC   ---------------------------------------------------------------------------
DR   EMBL; AF196304; AAF04852.1; -.
DR   EMBL; AF307849; AAG29931.1; -.
DR   EMBL; AF306508; AAG30253.1; -.
DR   EMBL; BC028583; AAH28583.1; -.
DR   EMBL; AK096455; BAC04794.1; -.
DR   EMBL; AB018340; BAA34517.2; ALT_INIT.
DR   MEROPS; C48.004; -.
DR   InterPro; IPR003653; Peptidase_C48.
DR   Pfam; PF02902; Peptidase_C48; 1.
DR   PROSITE; PS50600; ULP_PROTEASE; 1.
KW   Hydrolase; Protease; Thiol protease; Ubl conjugation pathway;
KW   Alternative splicing; Polymorphism.
FT   DOMAIN       666   1112       PROTEASE.
FT   ACT_SITE     765    765       BY SIMILARITY.
FT   ACT_SITE     917    917       BY SIMILARITY.
FT   ACT_SITE    1030   1030       BY SIMILARITY.
FT   VARSPLIC     153    159       Missing (in isoform 2).
FT                                /FTId=VSP_005274.
FT   VARIANT     1106   1106       Y -> C (in dbSNP:9250).
FT                                /FTId=VAR_016096.
FT   CONFLICT     121    121       T -> M (IN REF. 1, 6 AND 7).
FT   CONFLICT     293    293       D -> V (IN REF. 5).
FT   CONFLICT    1043   1043       Q -> E (IN REF. 1, 4, 6 AND 7).
SQ   SEQUENCE   1112 AA;  126144 MW;  B6E53875C3833A46 CRC64;

Query Match             46.0%;  Score 46;  DB 1;  Length 1112;
Best Local Similarity   47.4%;  Pred. No. 9.3;
Matches    9;  Conservative    3;  Mismatches    5;  Indels    2;  Gaps    1;

Qy        1 CASELGK--STNTFCKPPC 17
            |:|:|:|  |||:| | ||
Db      954 CSSEIGQWHLKPTICKQPC 972

RESULT 9
TIC1_MOUSE
ID   TIC1_MOUSE     STANDARD;      PRT;   442 AA.
AC   Q62288;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Testican-1 precursor (SPOCK protein).
GN   SPOCK OR SPOCK1 OR TICN1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=9624019; PubMed=8626787;
RA   Bonnet F., Perin J.-P., Charbonnier F., Camuzat A., Roussel G.,
RA   Nussbaum J.L., Alliel P.M.;
RT   "Structure and cellular distribution of mouse brain testican.
RT   Association with the postsynaptic area of hippocampus pyramidal
RT   cells.";
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RL   J. Biol. Chem. 271:4373-4380(1996).
CC   -!- FUNCTION: May play a role in cell-cell and cell-matrix
CC       interactions. May contribute to various neuronal mechanisms in the
CC       central nervous system.
CC   -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC   -!- TISSUE SPECIFICITY: Predominantly expressed in the postsynaptic
CC       area of pyramidal neurons.
CC   -!- PTM: Contains chondroitin sulfate and heparan sulfate O-linked
CC       oligosaccharides.
CC   -!- SIMILARITY: Contains 1 Kazal-like domain.
CC   -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; X92864; CAA63448.1; -.
DR   MGD; MGI:105371; Spock1.
DR   InterPro; IPR002350; kazal.
DR   InterPro; IPR000716; Thyroglobulin_1.
DR   Pfam; PF00050; kazal; 1.
DR   Pfam; PF00086; thyroglobulin_1; 1.
DR   SMART; SM00280; KAZAL; 1.
DR   SMART; SM00211; TY; 1.
DR   PROSITE; PS00484; THYROGLOBULIN_1; 1.
KW   Extracellular matrix; Proteoglycan; Heparan sulfate; Glycoprotein;
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    442       TESTICAN-1.
FT   DOMAIN      139    183       KAZAL-LIKE.
FT   DOMAIN      313    379       THYROGLOBULIN TYPE-I.
FT   DISULFID     89    100       BY SIMILARITY.
FT   DISULFID     94    110       BY SIMILARITY.
FT   DISULFID    139    169       BY SIMILARITY.
FT   DISULFID    142    162       BY SIMILARITY.
FT   DISULFID    151    183       BY SIMILARITY.
FT   CARBOHYD    386    386       O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT   CARBOHYD    391    391       O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
SQ   SEQUENCE    442 AA;  49541 MW;  818C30313F8ACOF6 CRC64;

Query Match             45.0%;  Score 45;  DB 1;  Length 442;
Best Local Similarity   50.0%;  Pred. No. 5.4;
Matches    8;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        2 ASELGKSTNTFCKPPC 17
            |||:| |||:||| ||
Db      168 ACSTGKSLNSLCDGPC 183

RESULT 10
RN30_RANPI
ID   RN30_RANPI     STANDARD;      PRT;   104 AA.
AC   P22069;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P-30 protein (EC 3.1.27.-) (Onconase).
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=91093131; PubMed=1985896;
RA   Ardelt W., Mikulski S.M., Shogen K.;
RT   "Amino acid sequence of an anti-tumor protein from Rana pipiens
RT   oocytes and early embryos. Homology to pancreatic ribonucleases.";
RL   J. Biol. Chem. 266:245-251(1991).
```

RN   [2]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=93066156; PubMed=1438177;
RA   Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
RA   James M.N.G.;
RT   "Comparative molecular modeling and crystallization of P-30 protein:
RT   a novel antitumor protein of Rana pipiens oocytes and early
RT   embryos.";
RL   Proteins 14:392-400(1992).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX   MEDLINE=94166079; PubMed=8120892;
RA   Mosimann S.C., Ardelt W., James M.N.G.;
RT   "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an
RT   amphibian ribonuclease with anti-tumor activity.";
RL   J. Mol. Biol. 236:1141-1153(1994).
CC   -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity
CC   against several tumor cell lines in vitro, as well as antitumor
CC   activity against high
CC   in vivo. It exhibits a ribonuclease-like activity against high
CC   molecular weight ribosomal RNA.
CC   -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PDB; 1ONC; 31-JAN-94.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES   1   1   PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE   10   10
FT   ACT_SITE   31   31
FT   ACT_SITE   97   97
FT   DISULFID   19   68
FT   DISULFID   30   75
FT   DISULFID   48   90
FT   DISULFID   87   104
FT   HELIX   3   10
FT   STRAND   11   12
FT   HELIX   19   22
FT   TURN   23   24
FT   TURN   26   30
FT   STRAND   33   38
FT   HELIX   41   45
FT   HELIX   46   48
FT   TURN   49   50
FT   STRAND   55   58
FT   STRAND   63   70
FT   TURN   74   75
FT   STRAND   77   84
FT   STRAND   86   91
FT   TURN   92   93
FT   STRAND   94   101
SQ   SEQUENCE   104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match   43.0%; Score 43; DB 1; Length 104;
Best Local Similarity   61.5%; Pred. No. 2.8;
Matches   8; Conservative   1; Mismatches   4; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFC 13
              :| |||| ||
Db   75 CKYKLKKSTNKFC 87

RESULT 11
EX22_ARATH
ID   EX22_ARATH   STANDARD;   PRT;   273 AA.
AC   Q9FL80;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Putative alpha-expansin 22 precursor (At-EXP22) (AtEx22) (Ath-

DE   ExpAlpha-1.15).
GN   EXP22 OR AT5G39270 OR K3K3.18 OR K3K3_120.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=98344145; PubMed=9679202;
RA   Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA   Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT   features of the regions of 1,381,565 bp covered by twenty one
RT   physically assigned P1 and TAC clones.";
RL   DNA Res. 5:131-145(1998).
RN   [2]
RP   CONCEPTUAL TRANSLATION.
RA   Cosgrove D.J.;
RL   Unpublished observations (DEC-2001).
CC   -!- FUNCTION: Causes loosening and extension of plant cell walls by
CC   disrupting noncovalent bonding between cellulose microfibrils and
CC   matrix glucans. No enzymatic activity has been found (By
CC   similarity).
CC   -!- SUBCELLULAR LOCATION: Cell-wall bound.
CC   -!- SIMILARITY: Belongs to the expansin family.
CC   -!- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC   -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC   -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC   gene model prediction.
CC   -!- DATABASE: NAME=EXPANSIN homepage;
CC   WWW="http://www.bio.psu.edu/expansins/".
CC   --
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CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; AB010694; BAB09382.1; ALT_SEQ.
DR   InterPro; IPR007112; Expan_endogl.
DR   InterPro; IPR007118; Expan_Lol_pI.
DR   InterPro; IPR007117; Expan_Lol_pI_C.
DR   Pfam; PF01357; Pollen_allergen; 1.
DR   PRINTS; PR01225; EXPANSNFAMLY.
DR   ProDom; PD002179; Expan_Lol_pI_C; 1.
DR   PROSITE; PS50843; EXPANSIN_CBD; 1.
DR   PROSITE; PS50842; EXPANSIN_EG45; 1.
KW   Hypothetical protein; Cell wall; Signal; Multigene family.
FT   SIGNAL   1   21   POTENTIAL.
FT   CHAIN   22   273   PUTATIVE ALPHA-EXPANSIN 22.
FT   DOMAIN   70   180   EXPANSIN-LIKE EG45.
FT   DOMAIN   190   269   EXPANSIN-LIKE CBD.
SQ   SEQUENCE   273 AA; 30219 MW; FA43411C2A543136 CRC64;

Query Match   43.0%; Score 43; DB 1; Length 273;
Best Local Similarity   37.5%; Pred. No. 7.3;
Matches   6; Conservative   4; Mismatches   6; Indels   0; Gaps   0;

Qy   1 CASELGKSTNTFCKPP 16
              ||:: |:|: :|||
Db   129 CPANYSKTTDLWCNPP 144

RESULT 12
EX26_ARATH
ID   EX26_ARATH   STANDARD;   PRT;   279 AA.
AC   Q9FI78;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)

```
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Putative alpha-expansin 26 precursor (At-EXP26) (AtEx26) (Ath-
DE   ExpAlpha-1.16).
GN   EXP26 OR AT5G39290 OR K3K3 20 OR K3K3 140.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=98344145; PubMed=9679202;
RA   Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA   Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT   features of the regions of 1,381,565 bp covered by twenty one
RT   physically assigned P1 and TAC clones.";
RL   DNA Res. 5:131-145(1998).
RN   [2]
RP   CONCEPTUAL TRANSLATION.
RA   Cosgrove D.J.;
RL   Unpublished observations (DEC-2001).
CC   -!- FUNCTION: Causes loosening and extension of plant cell walls by
CC       disrupting noncovalent bonding between cellulose microfibrils and
CC       matrix glucans. No enzymatic activity has been found (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cell-wall bound.
CC   -!- SIMILARITY: Belongs to the expansin family.
CC   -!- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC   -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC   -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC       gene model prediction.
CC   -!- DATABASE: NAME=EXPANSIN homepage;
CC       WWW="http://www.bio.psu.edu/expansin/".
CC   -------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------
DR   EMBL; AB010694; BAB09384.1; -.
DR   InterPro; IPR007112; Expan_endogl.
DR   InterPro; IPR007118; Expan_Lol_pI.
DR   InterPro; IPR007117; Expan_Lol_pI_C.
DR   Pfam; PF01357; Pollen_allergen; 1.
DR   PRINTS; PR01225; EXPANSNFAMLY.
DR   ProDom; PD002179; Expan_Lol_pI_C; 1.
DR   PROSITE; PS50179; Expan_Lol_pI_C; 1.
DR   PROSITE; PS50842; EXPANSIN_CBD; 1.
DR   PROSITE; PS50842; EXPANSIN_EG45; 1.
KW   Hypothetical protein; Cell wall; Signal; Multigene family.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    279       PUTATIVE ALPHA-EXPANSIN 26.
FT   DOMAIN       76    186       EXPANSIN-LIKE EG45.
FT   DOMAIN      196    275       EXPANSIN-LIKE CBD.
SQ   SEQUENCE   279 AA;  30980 MW;  5053E7C8497E47C4 CRC64;

Query Match             43.0%;  Score 43;  DB 1;  Length 279;
Best Local Similarity   37.5%;  Pred. No. 7.5;
Matches    6;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CASBLGKSTNTFCKPP 16
             |:|:.:|:| ||
Db     135 CPANYSKTTDLWCNPP 150


RESULT 13
ISPH_BUCAI
ID   ISPH_BUCAI    STANDARD;      PRT;   319 AA.
AC   P57247;
```

```
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2).
GN   ISPH OR LYTB OR BU147.
OS   Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS   symbiotic bacterium).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Buchnera.
OX   NCBI_TaxID=118099;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Tokyo 1998;
RX   MEDLINE=20445173; PubMed=10993077;
RA   Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT   "Genome sequence of the endocellular bacterial symbiont of aphids
RT   Buchnera sp. APS.";
RL   Nature 407:81-86(2000).
CC   -!- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
CC       into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate
CC       (DMAPP) (By similarity).
CC   -!- CATALYTIC ACTIVITY: Isopentenyl diphosphate + NAD(P)(+) + H(2)O =
CC       (E)-4-hydroxy-3-methylbut-2-en-1-yl diphosphate + NAD(P)H.
CC   -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
CC       (last) step.
CC   -!- SIMILARITY: Belongs to the ispH family.
CC   -------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------
DR   EMBL; AP001118; BAB12865.1; -.
DR   HAMAP; MF_00191; -; 1.
DR   InterPro; IPR003451; LytB.
DR   Pfam; PF02401; LYTB; 1.
DR   TIGRFAMs; TIGR00216; ispH_lytB; 1.
KW   Isoprene biosynthesis; Complete proteome; Oxidoreductase; NADP.
SQ   SEQUENCE   319 AA;  35741 MW;  69D8AFCC12DD09B8 CRC64;

Query Match             41.0%;  Score 41;  DB 1;  Length 319;
Best Local Similarity   66.7%;  Pred. No. 18;
Matches    8;  Conservative    1;  Mismatches    3;  Indels    0; -

Qy       3 SELGKSTNTFCK 14
             :|||||||| |
Db     232 AELGKETGTFTK 243


RESULT 14
CHIT_ARATH
ID   CHIT_ARATH    STANDARD;      PRT;   322 AA.
AC   P19171;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Basic endochitinase precursor (EC 3.2.1.14).
GN   AT3G12500 OR T2E22.18 OR T2E22 119 OR MQC3.32 OR MQC3.34.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RA   Samac D.A., Hironaka C.M., Yallaly P.E., Shah D.M.;
RT   "Isolation and characterization of the genes encoding basic and
RT   acidic chitinase in Arabidopsis thaliana.";
RL   Plant Physiol. 93:907-914(1990).
```

RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia.
RX   MEDLINE=20363099; PubMed=10907853;
RA   Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT   Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
RT   and BAC clones.";
RL   DNA Res. 7:217-221(2000).
CC   -!- FUNCTION: This protein functions as a defense against chitin
CC   containing fungal pathogens.
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC   acetyl-D-glucosamine polymers of chitin.
CC   -!- SUBCELLULAR LOCATION: Vacuolar and protoplast.
CC   -!- TISSUE SPECIFICITY: High constitutive level in roots with lower
CC   levels in leaves and flowering shoots.
CC   -!- INDUCTION: Ethylene induces high levels of systemic expression
CC   of basic chitinase with expression increasing with plant age.
CC   -!- SIMILARITY: Belongs to chitinase class IA (family 19 of glycosyl
CC   hydrolases).
CC   -!- SIMILARITY: Contains 1 chitin-binding type-1 domain.
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; M38240; AAA32769.1; ALT_INIT.
DR   EMBL; AP002047; BAB03157.1; -.
DR   HSSP; P23951; 2BAA.
DR   InterPro; IPR001002; Chitin_binding_1.
DR   InterPro; IPR000726; Glyco_hydro_19.
DR   Pfam; PF00187; Chitin_bind_1; 1.
DR   Pfam; PF00182; Glyco_hydro_19; 1.
DR   PRINTS; PR00451; CHITINBINDNG.
DR   ProDom; PD000609; Chitin_binding_1; 1.
DR   ProDom; PD354900; Glyco_hydro_19; 1.
DR   SMART; SM00270; ChtBD1; 1.
DR   PROSITE; PS50941; CHIT_BIND_I_2; 1.
DR   PROSITE; PS00026; CHIT_BIND_I; 1.
DR   PROSITE; PS00773; CHITINASE_19_1; 1.
DR   PROSITE; PS00774; CHITINASE_19_2; 1.
KW   Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal.
FT   SIGNAL   1   20
FT   CHAIN   21   315   BASIC ENDOCHITINASE.
FT   PROPEP   316   322   REMOVED IN MATURE FORM (PROBABLE).
FT   DOMAIN   21   62   CHITIN-BINDING TYPE-1.
FT   DISULFID   23   38   BY SIMILARITY.
FT   DISULFID   32   44   BY SIMILARITY.
FT   DISULFID   37   51   BY SIMILARITY.
FT   DISULFID   56   60   BY SIMILARITY.
FT   DISULFID   94   156   BY SIMILARITY.
FT   DISULFID   168   176   BY SIMILARITY.
FT   DISULFID   275   307   BY SIMILARITY.
SQ   SEQUENCE   322 AA; 34609 MW; C9AFFE4C544FCCD7 CRC64;

Query Match   41.0%; Score 41; DB 1; Length 322;
Best Local Similarity   50.0%; Pred No. 19;
Matches   9; Conservative   1; Mismatches   1; Indels   2; Gaps   1;

Qy   1 CASELGKSTNT--FCKPP 16
             |||| | | ||:|||
Db   37 CCSEFGWCGNTEPYCKQP 54

RESULT 15
ACK2_LISIN
ID   ACK2_LISIN   STANDARD;   PRT;   397 AA.
AC   Q92CN9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Acetate kinase 2 (EC 2.7.2.1) (Acetokinase 2).
GN   ACKA2 OR LIN1132.
OS   Listeria innocua.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=1642;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CLIP 11262 / Serovar 6a;
RX   MEDLINE=21537279; PubMed=11679669;
RA   Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA   Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA   Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA   Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA   Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA   Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA   Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA   Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA   Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA   Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA   Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT   "Comparative genomics of Listeria species.";
RL   Science 294:849-852(2001).
CC   -!- CATALYTIC ACTIVITY: ATP + acetate = ADP + acetyl phosphate.
CC   -!- PATHWAY: Conversion of acetate to acetyl-CoA; first step.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Belongs to the acetokinase family.
CC   -----
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CC   -----
DR   EMBL; AL596167; CAC96363.1; -.
DR   PIR; AC1574; AC1574.
DR   ListiList; LIN01132; -.
DR   HAMAP; MF_00020; -; 1.
DR   InterPro; IPR000890; Acetate_Kin.
DR   InterPro; IPR004372; AckA.
DR   Pfam; PF00871; Acetate_kinase; 1.
DR   PRINTS; PR00471; ACETATEKNASE.
DR   TIGRFAMs; TIGR00016; ackA; 1.
DR   PROSITE; PS01075; ACETATE_KINASE_1; 1.
DR   PROSITE; PS01076; ACETATE_KINASE_2; 1.
KW   Transferase; Kinase; Complete proteome.
SQ   SEQUENCE   397 AA; 43115 MW; 5822544EF92CBF51 CRC64;

Query Match   41.0%; Score 41; DB 1; Length 397;
Best Local Similarity   72.7%; Pred. No. 23;
Matches   8; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   1 CASELGKSTNT 11
             ||| |||| ||
Db   214 CAIEAGKSVNT 224

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OM protein - protein search, using sw model

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                                          (without alignments)
                                     139.448 Million cell updates/sec

Title:           US-09-761-636a-8
Perfect score:   100
Sequence:        1 CASELGKSTNTFCKPPC 17
Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:   1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  SPTREMBL_25:*
            1: sp_archea:*
            2: sp_bacteria:*
            3: sp_fungi:*
            4: sp_human:*
            5: sp_invertebrate:*
            6: sp_mammal:*
            7: sp_mhc:*
            8: sp_organelle:*
            9: sp_phage:*
           10: sp_plant:*
           11: sp_rodent:*
           12: sp_virus:*
           13: sp_vertebrate:*
           14: sp_unclassified:*
           15: sp_rvirus:*
           16: sp_bacteriap:*
           17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	Length	ID	Description
1	77	77.0	326	11	Q91ZE4	Q91ze4 rattus norv
2	61	61.0	252	13	Q8QGD7	Q8qgd7 gallus gall
3	59	59.0	326	11	Q91ZH6	Q91zh6 meriones un
4	59	59.0	415	11	Q91ZE3	Q91ze3 rattus norv
5	59	59.0	418	13	O57352	O57352 coturnix co
6	59	59.0	420	6	Q9XS50	Q9xs50 bos taurus
7	51.5	51.5	396	13	Q7T3I6	Q7t3i6 brachydanio
8	50	50.0	888	11	Q9CUD6	Q9cud6 mus musculu
9	50	50.0	891	11	Q8BJS7	Q8bjs7 mus musculu
10	49	49.0	127	13	Q9I8V8	Q9i8v8 rana pipien
11	48.5	48.5	746	10	Q8L791	Q8l791 arabidopsis
12	48.5	48.5	746	10	Q8LTJ8	Q8ltj8 arabidopsis
13	48	48.0	330	5	O18118	O18118 caenorhabdi
14	46	46.0	198	16	Q81WU7	Q81wu7 bacillus an
15	46	46.0	326	8	Q8MD06	Q8md06 leucaena gl
16	46	46.0	605	16	Q81JU8	Q81ju8 bacillus an
17	46	46.0	605	16	Q81AI0	Q81ai0 bacillus ce
18	45	45.0	86	17	Q8ZTL2	Q8ztl2 pyrobaculum
19	45	45.0	198	16	Q81A51	Q81a51 bacillus ce
20	45	45.0	364	11	Q8BM07	Q8bm07 mus musculu
21	45	45.0	367	10	Q9C6R6	Q9c6r6 arabidopsis
22	45	45.0	367	11	Q8BM19	Q8bm19 mus musculu
23	45	45.0	371	10	Q9C6F7	Q9c6f7 arabidopsis
24	45	45.0	439	11	Q8BKQ3	Q8bkq3 mus musculu
25	44.5	44.5	621	5	Q7YYH2	Q7yyh2 cryptospori
26	44.5	44.5	1036	5	Q81BS4	Q81bs4 plasmodium
27	44	44.0	145	5	Q9VE57	Q9ve57 drosophila
28	44	44.0	193	5	Q8TA40	Q8ta40 heterodera
29	44	44.0	461	16	Q8D4T1	Q8d4t1 vibrio vuln
30	44	44.0	471	10	Q9FHK1	Q9fhk1 arabidopsis
31	44	44.0	677	5	Q9FLD9	Q9fld9 arabidopsis
32	44	44.0	1189	5	Q9W378	Q9w378 drosophila
33	44	44.0	1189	5	Q9Y1I1	Q9y1i1 drosophila
34	43	43.0	1717	5	Q26566	Q26566 schistosoma
35	43	43.0	100	16	Q92KW0	Q92kw0 helicobacte
36	43	43.0	127	13	Q8UVX5	Q8uvx5 rana pipien
37	43	43.0	603	16	Q8R6T0	Q8r6t0 thermoanaer
38	43	43.0	693	3	Q08001	Q08001 saccharomyc
39	43	43.0	849	4	Q96SQ3	Q96sq3 homo sapien
40	43	43.0	997	5	Q967Z1	Q967z1 trypanosoma
41	42	42.0	175	5	Q9LKW0	Q9lkw0 lycopersico
42	42	42.0	288	5	Q9XYV5	Q9xyv5 toxocara ca
43	42	42.0	326	10	P93680	P93680 persea amer
44	42	42.0	1011	3	Q9P944	Q9p944 pneumocysti
45	42	42.0	1428	5	O44341	O44341 haliotis ru

ALIGNMENTS

```
RESULT 1
Q91ZE4
ID   Q91ZE4       PRELIMINARY;       PRT;   326 AA.
AC   Q91ZE4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   VEGF-D.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Kirkin V.; Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,
RA   Pepper M.S., Giannis A., Sleeman J.P.;
RT   "Characterization of indolinones which specifically inhibit VEGF-C and
RT   VEGF-D-induced activation of VEGFR-3 but not VEGFR-2.";
RL   Eur. J. Biochem. 0:0-0(2001).
DR   EMBL; AY032728; AAK96008.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 1.
DR   Pfam; PF03341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE 326 AA; 37106 MW; D7CAEBA6C9FABB7D CRC64;

Query Match       77.0%;        Score 77;  DB 11;  Length 326;
Best Local Similarity   87.5%;        Pred. No. 1.9e-05;
Matches   14;   Conservative   1;   Mismatches   1;   Indels   0;   Gaps   0;

Qy        2 ASELGKSTNTFCKPPC 17
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Db       ||||||:||||| ||||
         126 ASELGKTTNTFFKPPC 141


RESULT 2
Q8QGD7
ID   Q8QGD7         PRELIMINARY;       PRT;   252 AA.
AC   Q8QGD7;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor D.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Diaz-Trelles R., Rodriguez-Leon J., Kawakami Y.,
RA   Izpisua-Belmonte J.C.;
RT   "Expression of the chick vascular endothelial growth factor D gene
RT   during limb development.";
RL   Mech. Dev. 0:0-0(2002).
DR   EMBL; AF479650; AAM12733.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   252 AA;  28767 MW;  64347SDAB2B72F27 CRC64;

Query Match             61.0%;  Score 61;  DB 13;  Length 252;
Best Local Similarity   68.8%;  Pred. No. 0.011;
Matches  11;  Conservative   1;  Mismatches   4;  Indels   0;  Gaps   0;

Qy        2 ASELGKSTNTFCKPPC 17
            | |||:||  |||||
Db      121 AKELGTTTNKFFKPPC 136


RESULT 3
Q91ZH6
ID   Q91ZH6         PRELIMINARY;       PRT;   326 AA.
AC   Q91ZH6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor C (Fragment).
GN   VEGFC.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Panilaitis B.J., Fuhrman J.A.;
RT   "Brugia malayi stimulates VEGF-C, a growth factor specific for
RT   lymphatic endothelium, by an indirect mechanism.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF432867; AAL28127.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
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DR   Pfam; PF03128; CXCXC; 5.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   326 AA;  36826 MW;  D0B2772C77836914 CRC64;

Query Match             59.0%;  Score 59;  DB 11;  Length 326;
Best Local Similarity   71.4%;  Pred. No. 0.033;
Matches  10;  Conservative   1;  Mismatches   3;  Indels   0;  Gaps   0;

Qy        4 ELGKSTNTFCKPPC 17
            | |||| ||||||
Db       50 EFGAATNTFFKPPC 63


RESULT 4
Q91ZE3
ID   Q91ZE3         PRELIMINARY;       PRT;   415 AA.
AC   Q91ZE3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   VEGF-C.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,
RA   Pepper M.S., Giannis A., Sleeman J.P.;
RT   "Characterization of indolinones which specifically inhibit VEGF-C-and
RT   VEGF-D-induced activation of VEGFR-3 but not VEGFR-2.";
RL   Eur. J. Biochem. 0:0-0(2001).
DR   EMBL; AY032729; AAK96009.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 5.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   415 AA;  46397 MW;  1EB677F5B260A525 CRC64;

Query Match             59.0%;  Score 59;  DB 11;  Length 415;
Best Local Similarity   71.4%;  Pred. No. 0.042;
Matches  10;  Conservative   1;  Mismatches   3;  Indels   0;  Gaps   0;

Qy        4 ELGKSTNTFCKPPC 17
            | :|||| ||||||
Db      139 EFGAATNTFFKPPC 152


RESULT 5
O57352
ID   O57352         PRELIMINARY;       PRT;   418 AA.
AC   O57352;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor C precursor.
GN   VEGF-C.
```

OS   Coturnix coturnix (Common quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=9091;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98167900; PubMed=9435294;
RA   Eichmann A., Corbel C., Jaffredo T., Breant V., Joukov V., Kumar V.,
RA   Alitalo K., Le Douarin N.M.;
RT   "Avian VEGF-C: cloning, embryonic expression pattern and stimulation
RT   of the differentiation of VEGFR2 expressing endothelial cell
RT   precursors.";
RL   Development 125:743-752(1998).
DR   EMBL; Y15837; CAA75799.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 6.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Signal.
FT   SIGNAL   1   31
FT   CHAIN   111   418   VASCULAR ENDOTHELIAL GROWTH FACTOR C.
SQ   SEQUENCE   418 AA; 46839 MW; 099BFCC79151BF2B CRC64;

Query Match   59.0%; Score 59; DB 13; Length 418;
Best Local Similarity   71.4%; Pred. No. 0.043;
Matches   10; Conservative   1; Mismatches   3; Indels   0; Gaps   0;

Qy   4 ELGKSTNTFCKPPC 17
               | :||||| ||||
Db   142 EFGAATNTFFKPPC 155

RESULT 6
Q9XS50
ID   Q9XS50   PRELIMINARY;   PRT;   420 AA.
AC   Q9XS50;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor C precursor.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=20044783; PubMed=10575000;
RA   Yonekura H., Sakurai S., Liu X., Migita H., Wang H., Yamagishi S.,
RA   Nomura M., Abedin M.J., Unoki H., Yamamoto Y., Yamamoto H.;
RT   "Placenta growth factor and vascular endothelial growth factor B and C
RT   expression in microvascular endothelial cells and pericytes.
RT   Implication in autocrine and paracrine regulation of angiogenesis.";
RL   J. Biol. Chem. 274:35172-35178(1999).
DR   EMBL; AB004275; BAA77687.1; -.
DR   HSSP; P01127; 1PDG.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR002400; GF_cysknot.

DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 5.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Signal.
FT   SIGNAL   1   20   POTENTIAL.
FT   CHAIN   21   420   VASCULAR ENDOTHELIAL GROWTH FACTOR C.
SQ   SEQUENCE   420 AA; 46681 MW; 58BA84317A3C8E2D CRC64;

Query Match   59.0%; Score 59; DB 6; Length 420;
Best Local Similarity   71.4%; Pred. No. 0.043;
Matches   10; Conservative   1; Mismatches   3; Indels   0; Gaps   0;

Qy   4 ELGKSTNTFCKPPC 17
               | :||||| ||||
Db   144 EFGAATNTFFKPPC 157

RESULT 7
Q7T3I6
ID   Q7T3I6   PRELIMINARY;   PRT;   396 AA.
AC   Q7T3I6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vascular endothelial growth factor C.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Olofsson B., Ober E.A., Makinen T., Jin S.-W., Shoji W., Koh G.Y.,
RA   Alitalo K., Stainier D.Y.R.;
RT   "vascular endothelial growth factor C regulates endodermal
RT   morphogenesis in zebrafish.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF466147; AAP44161.1; -.
SQ   SEQUENCE   396 AA; 45287 MW; C20F9B3F0307D7C1 CRC64;

Query Match   51.5%; Score 51.5; DB 13; Length 396;
Best Local Similarity   58.8%; Pred. No. 0.9;
Matches   10; Conservative   3; Mismatches   3; Indels   1; Gaps   1;

Qy   4 ELGK--STNTFCKPPC 17
               ::|| :||||| ||||
Db   127 DVGKEFGATNTFYKPPC 143

RESULT 8
Q9CUD6
ID   Q9CUD6   PRELIMINARY;   PRT;   888 AA.
AC   Q9CUD6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Adult male testis cDNA, RIKEN full-length enriched library,
DE   clone:4933403G14 product:hypothetical serine-rich region containing
DE   protein, full insert sequence (Fragment).
GN   4933403G14RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
DR   EMBL; AK016632; BAB30348.2; -.
DR   PIR; PT0546; PT0698.
DR   MGD; MGI:1921643; 4933403G14Rik.
KW   Hypothetical protein.
FT   NON_TER   888   888
SQ   SEQUENCE   888 AA;   95846 MW;   E42D3971F1F95484 CRC64;

Query Match   50.0%; Score 50; DB 11; Length 888;
Best Local Similarity   64.3%; Pred. No. 3.9;
Matches   9; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   3 SELGKSTNTFCKPP 16
                :|| |||||||
Db   259 TELDFETNTFCPPP 272

RESULT 9
Q8BJS7
ID   Q8BJS7   PRELIMINARY;   PRT;   891 AA.
AC   Q8BJS7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical serine-rich region containing protein.
GN   4933403G14Rik.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK080043; BAC37814.1; -.
DR   PIR; PT0546; PT0698.
DR   PIR; PT0645; PT0645.
DR   MGD; MGI:1921643; 4933403G14Rik.
KW   Hypothetical protein.
SQ   SEQUENCE   891 AA;   96154 MW;   471D83C532E85A55 CRC64;

Query Match   50.0%; Score 50; DB 11; Length 891;
Best Local Similarity   64.3%; Pred. No. 3.9;
Matches   9; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   3 SELGKSTNTFCKPP 16
                :|| |||||||
Db   260 TELDFETNTFCPPP 273

RESULT 10
Q918V8
ID   Q918V8   PRELIMINARY;   PRT;   127 AA.
AC   Q918V8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase variant rapLR1 precursor.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20330357; PubMed=10871370;
RA   Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT   "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT   3' UTR of unusual length and structure.";
RL   Nucleic Acids Res. 28:2375-2382(2000).
DR   EMBL; AF165133; AAF76935.1; -.
DR   PIR; A39035; A39035.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNase_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL   1   23   POTENTIAL.
SQ   SEQUENCE   127 AA;   14491 MW;   B8511DC5407AB69B CRC64;

Query Match   49.0%; Score 49; DB 13; Length 127;

```
Best Local Similarity   69.2%;   Pred. No. 0.79;
Matches   9;   Conservative   1;   Mismatches   3;   Indels   0;   Gaps   0;

Qy    1 CASELGKSTNTFC 13
        :.| |||||||
Db   98 CKYKLKKSTNTFC 110
```

```
RESULT 11
ID   Q9LTJ8
AC   Q9LTJ8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Genomic DNA, chromosome 5, BAC clone:F17P19.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Columbia;
RA   Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA   Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB025603; BAA97466.1; -.
SQ   SEQUENCE   746 AA;   82656 MW;   A0EACB409EB5953A CRC64;
```

```
Query Match        48.5%;   DB 10;   Length 746;
Best Local Similarity   35.7%;   Pred. No. 6;
Matches   10;   Conservative   3;   Mismatches   3;   Indels   4;   Gaps   1;

Qy    1 CASELGKSTNTF------------CKPPC 17
        |:.:.|||||:|            |||
Db  583 CSEVMEKSTNSFSSAFDSTLADLCKDPC 610
```

```
RESULT 12
ID   Q8L791
AC   Q8L791;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
GN   ATSG52230.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA   Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA   Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
RA   Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
RA   Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,
RA   Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
RA   Theologis A., Davis R.W.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA   Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA   Cheuk R., Chung M.K., Bowser L., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA   Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA   Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA   Ecker J., Theologis A., Davis R.W.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY136403; AAM97069.1; -.
DR   EMBL; BT000226; AAN15545.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   746 AA;   82598 MW;   D3E6FBB7C916L084 CRC64;
```

```
Query Match        48.5%;   DB 10;   Length 746;
Best Local Similarity   35.7%;   Pred. No. 6;
Matches   10;   Conservative   3;   Mismatches   4;   Indels   11;   Gaps   1;

Qy    1 CASELGKSTNTF------------CKPPC 17
        |:.:.|||||:|            |||
Db  583 CSEVMEKSTNSFSSAFDSTLADLCKDPC 610
```

```
RESULT 13
ID   O18118
AC   O18118;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   T23F1.6 protein.
GN   T23F1.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilkinson J.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z81129; CAB03405.1; -.
DR   PIR; T25169; T25169.
DR   WormPep; T23F1.6; CE14080.
DR   InterPro; IPR003341; DUF139.
DR   Pfam; PF02363; C_triplex; 8.
SQ   SEQUENCE   330 AA;   36605 MW;   F043B1A90D3A8FE9 CRC64;
```

```
Query Match        48.0%;   DB 5;   Length 330;
Best Local Similarity   41.2%;   Pred. No. 3.2;
Matches   7;   Conservative   4;   Mismatches   6;   Indels   0;   Gaps   0;

Qy    1 CASELGKSTNTFCKPPC 17
        |:.:.||| :|:|
Db   80 CSQQCQSNTNTQCQPTC 96
```

```
RESULT 14
ID   Q81WU7
AC   Q81WU7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ada regulatory protein/6-O-methylguanine-DNA methyltransferase.
GN   ADAA OR BA3869.
OS   Bacillus anthracis (strain Ames).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=198094;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22608414; PubMed=12721629;
RA   Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA   Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA   Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA   Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
```

RA   DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA   Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA   Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA   Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA   Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA   Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA   Fraser C.M.;
RT   "The genome sequence of Bacillus anthracis Ames and comparison to
RT   closely related bacteria.";
RL   Nature 423:81-86(2003).
DR   EMBL; AE017036; AAP27604.1; -.
DR   TIGR; BA3869; -.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0008168; F:methyltransferase activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006281; P:DNA repair; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR004026; Ada_Zn_bind.
DR   InterPro; IPR000005; HTHAraC.
DR   Pfam; PF02805; Ada_Zn_binding; 1.
DR   Pfam; PF00165; HTH_AraC; 2.
DR   PRINTS; PR00032; HTHARAC.
DR   SMART; SM00342; HTH_ARAC; 1.
DR   PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR   PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW   Methyltransferase; Transferase; Complete proteome.
SQ   SEQUENCE 198 AA; 23280 MW; ABBEC1A5A353170A CRC64;

Query Match   46.0%; Score 46; DB 16; Length 198;
Best Local Similarity 63.6%; Pred. No. 4.3;
Matches   7; Conservative   1; Mismatches   1; Indels   3; Gaps   0;

Qy   7 KSTNTFCKPPC 17
            ||| ||:||
Db   32 KSTGVFCRPSC 42

RESULT 15
QBMD06
ID   Q8MD06   PRELIMINARY;   PRT;   326 AA.
AC   Q8MD06;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Chitinase.
OS   Leucaena glauca (White popinac) (Leucaena leucocephala).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Fabales; Fabaceae; Mimosoideae; Mimoseae; Leucaena.
OX   NCBI_TaxID=3866;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ketudat-Cairns J.R., Mizuno K., Fujimura T., Sriyotha P.;
RT   "Cloning, Expression, and Characterization of an Anti-fungal Chitinase
RT   from Leucaena leucocephala de Wit.";
RL   Biosci. Biotechnol. Biochem. 0:0-0(2002).
DR   EMBL; AF513017; AAM49597.2; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
DR   GO; GO:0008061; F:chitin binding; IEA.
DR   GO; GO:0004568; F:chitinase activity; IEA.
DR   GO; GO:0016998; P:cell wall catabolism; IEA.
DR   GO; GO:0006032; P:chitin catabolism; IEA.
DR   GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.
DR   InterPro; IPR001002; Chitin_binding_1.
DR   InterPro; IPR000726; Glyco_hydro_19.
DR   Pfam; PF00187; Chitin_bind_1; 1.
DR   Pfam; PF00182; Glyco_hydro_19; 1.
DR   PRINTS; PR00451; CHITINBINDNG.
DR   ProDom; PD000609; Chitin_binding_1; 1.
DR   ProDom; PD354900; Glyco_hydro_19; 1.
DR   SMART; SM00270; ChtBD1; 1.
DR   PROSITE; PS00773; CHITINASE_19_1; 1.
DR   PROSITE; PS00774; CHITINASE_19_2; 1.
DR   PROSITE; PS00026; CHITIN_BINDING; 1.
KW   Chitin-binding; Chloroplast.
SQ   SEQUENCE 326 AA; 34908 MW; F735142684A84A46D CRC64;

Query Match   46.0%; Score 46; DB 8; Length 326;
Best Local Similarity 47.4%; Pred. No. 7.2;
Matches   9; Conservative   2; Mismatches   6; Indels   2; Gaps   1;

Qy   1 CASELG--KSTNTFCKPPC 17
            ||:|| | |||:|||
Db   41 CCSQFGWCGSTNDYCGPGC 59

Search completed: September 5, 2004, 09:59:58
Job time : 40.4646 secs

OM protein - protein search, using sw model

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Run on: September 5, 2004, 09:37:49 ; Search time 55.8081 Seconds
                 (without alignments)
                 86.068 Million cell updates/sec

Title: US-09-761-636A-8
Perfect score: 100
Sequence: 1 CASELGKSTNTFCKPPC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_29Jan04.*
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                 2: geneseqp1990s.*
                 3: geneseqp2000s.*
                 4: geneseqp2001s.*
                 5: geneseqp2002s.*
                 6: geneseqp2003as.*
                 7: geneseqp2003bs.*
                 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	100	100.0	17	4	AAU04527	Aau04527 VEGF base
2	97	97.0	17	4	AAU04550	Aau04550 VEGF base
3	97	97.0	17	4	AAU04546	Aau04546 VEGF base
4	93	93.0	17	4	AAU04547	Aau04547 VEGF base
5	93	93.0	17	4	AAU04551	Aau04551 VEGF base
6	93	93.0	17	4	AAU04549	Aau04549 VEGF base
7	89	89.0	17	4	AAU04548	Aau04548 VEGF base
8	80	80.0	73	4	AAU04522	Aau04522 Human VEG
9	80	80.0	96	4	AAU04520	Aau04520 Human VEG
10	80	80.0	109	3	AAY23889	Aay23889 Human vas
11	80	80.0	109	3	AAB11931	Aab11931 Human tru
12	80	80.0	109	6	ABB84621	Abb84621 Human wil
13	80	80.0	109	6	ABG73750	Abg73750 Human VEG
14	80	80.0	287	6	ABG73779	Abg73779 Human NVR
15	80	80.0	325	2	AAW53240	Aaw53240 Homo sapi
16	80	80.0	325	4	AAY97572	Aay97572 Human VEG
17	80	80.0	354	2	AAW44293	Aaw44293 Human vas
18	80	80.0	354	2	AAW49036	Aaw49036 Human zve
19	80	80.0	354	2	AAW53241	Aaw53241 Homo sapi
20	80	80.0	354	3	AAB10649	Aab10649 Human VEG
21	80	80.0	354	3	AAY70750	Aay70750 Human pre
22	80	80.0	354	3	AAY70983	Aay70983 Human vas
23	80	80.0	354	4	AAB29049	Aab29049 Human VEG
24	80	80.0	354	4	AAB37606	Aab37606 Human VEG
25	80	80.0	354	4	AAB70685	Aab70685 Human vas
26	80	80.0	354	4	AAY97573	Aay97573 Human VEG
27	80	80.0	354	4	AAU08441	Aau08441 Polypepti
28	80	80.0	354	5	ABG33055	Abg33055 Human vas
29	80	80.0	354	5	ABG32046	Abg32046 Human Flt
30	80	80.0	354	6	ABB84623	Abb84623 Human VEG
31	80	80.0	354	7	ADD08950	Add08950 Human VEG
32	80	80.0	620	2	AAW14994	Aaw14994 Human C-F
33	77	77.0	110	5	AAM47933	Aam47933 Mouse VEG
34	77	77.0	178	2	AAY08287	Aay08287 Human gro
35	77	77.0	321	2	AAW53243	Aaw53243 Mus muscu
36	77	77.0	321	5	AAM47931	Aam47931 Mouse VEG
37	77	77.0	326	2	AAW44296	Aaw44296 Rat vascu
38	77	77.0	337	2	AAY08286	Aay08286 Human gro
39	77	77.0	358	2	AAW14992	Aaw14992 Murine c-
40	77	77.0	358	2	AAW44295	Aaw44295 Mouse vas
41	77	77.0	358	2	AAW53242	Aaw53242 Mus muscu
42	77	77.0	358	5	AAM47930	Aam47930 Mouse VEG
43	72	72.0	13	4	AAU04524	Aau04524 VEGF base
44	69	69.0	13	4	AAU04534	Aau04534 VEGF base
45	65	65.0	13	4	AAU04535	Aau04535 VEGF base

ALIGNMENTS

RESULT 1
AAU04527
ID   AAU04527 standard; protein; 17 AA.
XX
AC   AAU04527;
XX
DT   26-SEP-2001 (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #1.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Disulfide-bond 1..13
FT   /note= "This bond cyclises the peptide"
FT   Disulfide-bond 17
FT   /note= "A disulfide bond forms between residue 17 and
FT   residue 17 of an identical peptide to form a dimeric
FT   peptide, or to residue 1 of the sequence appearing as
FT   AAU04528, also forming a dimeric peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Claim 59; Page 32; 102pp; English.
XX

```
CC   The sequence represents a dimeric bicyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 17 AA;

Query Match             100.0%;  Score 100; DB 4; Length 17;
Best Local Similarity   100.0%;  Pred. No. 6.2e-08;
Matches  17;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 CASELGKSTNTFCKPPC 17
       |||||||||||||||||
Db   1 CASELGKSTNTFCKPPC 17

RESULT 2
AAU04550
ID   AAU04550 standard; peptide; 17 AA.
XX
AC   AAU04550;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #7.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  1..13
FT                   /note= "This bond cyclises the peptide"
FT   Disulfide-bond  17
FT                   /note= "A disulfide bond forms between residue 17 and
FT                   residue 1 of the sequence appearing as AAU04528, forming
FT                   a dimeric peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX

PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 26; Page 49; 102pp; English.
XX
CC   The sequence represents a dimeric bicyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human,
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 17 AA;

Query Match             97.0%;  Score 97; DB 4; Length 17;
Best Local Similarity   94.1%;  Pred. No. 1.7e-07;
Matches  16;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 CASELGKSTNTFCKPPC 17
       ||||||||||| |||||
Db   1 CASELGKSTNTYCKPPC 17

RESULT 3
AAU04546
ID   AAU04546 standard; peptide; 17 AA.
XX
AC   AAU04546;
XX
DT   26-SEP-2001  (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #3.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  1..13
FT                   /note= "This bond cyclises the peptide"
FT   Disulfide-bond  17
```

```
FT           /note= "A disulfide bond forms between residue 17 and
FT           residue 17 of an identical peptide to form a dimeric
FT           peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 26; Page 49; 102pp; English.
XX
CC   The sequence represents a dimeric bicyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 17 AA;

Query Match      97.0%;   Score 97;  DB 4;  Length 17;
Best Local Similarity    94.1%;   Pred. No. 1.7e-07;
Matches  16;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 CASELGKSTNTFCKPPC 17
            |:|||||||||||||||
Db      1 CATELGKSTNTFCKPPC 17

RESULT 4
AAU04547
ID   AAU04547 standard; peptide; 17 AA.
XX
AC   AAU04547;
XX
DT   26-SEP-2001 (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #4.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key        Location/Qualifiers
FT   Disulfide-bond   1..13
FT              /note= "This bond cyclises the peptide"
FT   Disulfide-bond   17
FT              /note= "A disulfide bond forms between residue 17 and
FT              residue 17 of an identical peptide to form a dimeric
FT              peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 26; Page 49; 102pp; English.
XX
CC   The sequence represents a dimeric bicyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 17 AA;

Query Match      93.0%;   Score 93;  DB 4;  Length 17;
Best Local Similarity    88.2%;   Pred. No. 6.9e-07;
Matches  15;  Conservative   2;  Mismatches   0;  Indels   0;  Gaps   0;
```

```
Qy    1 CASELGKSTNTFCKPPC 17
        |||||||::|||||||||
Db    1 CASELGKTSNTFCKPPC 17

RESULT 5
AAU04551
ID   AAU04551 standard; peptide; 17 AA.
XX
AC   AAU04551;
XX
DT   26-SEP-2001 (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #8.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Disulfide-bond 1..13
FT                  /note= "This bond cyclises the peptide"
FT   Disulfide-bond 17
FT                  /note= "A disulfide bond forms between residue 17 and
FT                  residue 1 of the sequence appearing as AAU04528, forming
FT                  a dimeric peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 26; Page 49; 102pp; English.
XX
CC   The sequence represents a dimeric bicyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,

CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 17 AA;

Query Match             93.0%;  Score 93; DB 4; Length 17;
Best Local Similarity   88.2%;  Pred. No. 6.9e-07;
Matches   15;  Conservative  2;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 CASELGKSTNTFCKPPC 17
        |||||||::|||:|||||
Db    1 CASELGRSTNSFCKPPC 17

RESULT 6
AAU04549
ID   AAU04549 standard; peptide; 17 AA.
XX
AC   AAU04549;
XX
DT   26-SEP-2001 (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #6.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Disulfide-bond 1..13
FT                  /note= "This bond cyclises the peptide"
FT   Disulfide-bond 17
FT                  /note= "A disulfide bond forms between residue 17 and
FT                  residue 17 of an identical peptide to form a dimeric
FT                  peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 26; Page 49; 102pp; English.
XX
CC   The sequence represents a dimeric bicyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
```

CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 17 AA;

Query Match   93.0%; Score 93; DB 4; Length 17;
Best Local Similarity   88.2%; Pred. No. 6.9e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CASELGKSTNTFCKPPC 17
        |||||:||||:|:|||||
Db   1 CASELGRSTNSFCKPPC 17

RESULT 7
AAU04548
ID   AAU04548 standard; peptide; 17 AA.
XX
AC   AAU04548;
XX
DT   26-SEP-2001 (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #5.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Disulfide-bond 1..13
FT   /note= "This bond cyclises the peptide"
FT   Disulfide-bond 17
FT   /note= "A disulfide bond forms between residue 17 and
FT   residue 17 of an identical peptide to form a dimeric
FT   peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 26; Page 49; 102pp; English.
XX
CC   The sequence represents a dimeric bicyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides; dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 17 AA;

Query Match   89.0%; Score 89; DB 4; Length 17;
Best Local Similarity   82.4%; Pred. No. 2.7e-06;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CASELGKSTNTFCKPPC 17
        |||::||||||:|||||
Db   1 CASDVGKSTNTWCKPPC 17

RESULT 8
AAU04522
ID   AAU04522 standard; protein; 73 AA.
XX
AC   AAU04522;
XX
DT   26-SEP-2001 (first entry)
XX
DE   Human VEGF-D amino acids Val101-Thr 173.
XX
KW   Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;

XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 1; Page 90-91; 102pp; English.
XX
CC   The sequence represents Human VEGF-D (vascular endothelial growth factor)
CC   amino acids Val101-Thr 173, used together with the C-terminal 23 residues
CC   of VEGF to make a hybrid theoretical molecule for 3 dimensional
CC   modelling. The sequence is used in a method of producing a monomeric
CC   monocyclic peptide by a measuring beta-beta carbon separation distances
CC   on opposite antiparallel strands of a peptide loop fragment from an
CC   exposed loop of a growth factor protein and cyclising the peptide by
CC   oxidising the cysteine residues. The monocyclic peptides, dimeric
CC   bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
CC   peptide with at least one amino acid deleted prior to cyclisation are
CC   used to interfere with angiogenesis, neovascularisation or
CC   lymphangiogenesis in a mammal with a condition characterised by
CC   angiogenesis, neovascularisation or lymphangiogenesis. The condition is
CC   diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
CC   malignant or benign tumour, post-recovery cerebrovascular accident, post-
CC   angioplasty restenosis, head, heat or cold trauma, substance-induced
CC   neovascularisation of the liver, excessive hormone-related angiogenic
CC   dysfunction, diabetes induced neovascular sequelae, hypertension induced
CC   neovascular sequelae, or chronic liver infection. The peptides are also
CC   used to modulate vascular permeability in a mammal (the mammal has a
CC   condition characterised by fluid accumulation in peripheral limbs or in
CC   lungs, peritoneal cavity, pleura, or brain. The peptides are used to
CC   image blood vessels and lymphatic vasculature. The monomeric and bicyclic
CC   peptides are used to interfere with at least one biological activity
CC   induced by VEGF, VEGF-C or -D and are also used in combination with an
CC   anti-inflammatory agent, to treat a chronic inflammation, especially
CC   rheumatoid arthritis, psoriasis and diabetic retinopathy
XX
SQ   Sequence 73 AA;

Query Match   80.0%;   Score 80; DB 4; Length 73;
Best Local Similarity 93.8%;   Pred. No. 0.00024;
Matches 15;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   2 ASELGKSTNTFCKPPC 17
            ||||||||||| ||||
Db   21 ASELGKSTNTFFKPPC 36

RESULT 9
AAU04520
ID   AAU04520 standard; protein; 96 AA.
XX
AC   AAU04520;
XX
DT   26-SEP-2001   (first entry)
XX
DE   Human VEGF-D amino acids Val101-PRO186.
XX
KW   Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
PR   18-JAN-2000; 2000US-0176293P.

PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 1; Page 89; 102pp; English.
XX
CC   The sequence represents Human VEGF-D (vascular endothelial growth factor)
CC   amino acids Val101-PRO186. The sequence is used in a method of producing
CC   a monomeric monocyclic peptide by a measuring beta-beta carbon separation
CC   distances on opposite antiparallel strands of a peptide loop fragment
CC   from an exposed loop of a growth factor protein and cyclising the peptide
CC   by oxidising the cysteine residues. The monocyclic peptides, dimeric
CC   bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
CC   peptide with at least one amino acid deleted prior to cyclisation are
CC   used to interfere with angiogenesis, neovascularisation or
CC   lymphangiogenesis in a mammal with a condition characterised by
CC   angiogenesis, neovascularisation or lymphangiogenesis. The condition is
CC   diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
CC   malignant or benign tumour, post-recovery cerebrovascular accident, post-
CC   angioplasty restenosis, head, heat or cold trauma, substance-induced
CC   neovascularisation of the liver, excessive hormone-related angiogenic
CC   dysfunction, diabetes induced neovascular sequelae, hypertension induced
CC   neovascular sequelae, or chronic liver infection. The peptides are also
CC   used to modulate vascular permeability in a mammal (the mammal has a
CC   condition characterised by fluid accumulation in peripheral limbs or in
CC   lungs, peritoneal cavity, pleura, or brain. The peptides are used to
CC   image blood vessels and lymphatic vasculature. The monomeric and bicyclic
CC   peptides are used to interfere with at least one biological activity
CC   induced by VEGF, VEGF-C or -D and are also used in combination with an
CC   anti-inflammatory agent, to treat a chronic inflammation, especially
CC   rheumatoid arthritis, psoriasis and diabetic retinopathy
XX
SQ   Sequence 96 AA;

Query Match   80.0%;   Score 80; DB 4; Length 96;
Best Local Similarity 93.8%;   Pred. No. 0.00031;
Matches 15;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   2 ASELGKSTNTFCKPPC 17
            ||||||||||| ||||
Db   21 ASELGKSTNTFFKPPC 36

RESULT 10
AAY23889
ID   AAY23889 standard; protein; 109 AA.
XX
AC   AAY23889;
XX
DT   21-SEP-1999   (first entry)
XX
DE   Human vascular endothelial growth factor (VEGF)-D.
XX
KW   vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma;
KW   tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft;
KW   wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.
XX
OS   Homo sapiens.
XX
PN   WO993485-A1.
XX
PD   08-JUL-1999.
XX
PF   23-DEC-1998;   98WO-US027373.

XX
PR   24-DEC-1997;   97AU-00001131.
PR   29-MAY-1998;   98US-0087392P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Stacker SA, Alitalo K;
XX
DR   WPI; 1999-405368/34.
XX
PT   A human cell line stably expressing vascular endothelial growth factor D,
PT   useful for treating melanomas or tumors expressing VEGF-D.
XX
PS   Claim 6; Page 72; 79pp; English.
XX
CC   The present sequence represents human vascular endothelial growth factor
CC   (VEGF)-D. The specification describes a human cell line which stably
CC   expresses VEGF-D, or fragments/analogues having VEGF-D biological
CC   activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex
CC   DNA, VEGF-D variants or antibodies (especially chimeric antibodies), are
CC   useful for the treatment or alleviation of malignant melanomas, tumours
CC   or psoriasis. Angiogenesis and lymphangiogenesis stimulating amounts of
CC   VEGF-D can be administered to enhance the acceptance and/or healing of
CC   skin grafts or to stimulate the healing of a surgical or traumatic wound
CC   to the skin. Lymphangiogenesis stimulating amounts of VEGF-D can be used
CC   to treat lymphedema. Endothelial proliferation stimulating amounts of
CC   VEGF-D are used to treat scleroderma. Vascularisation stimulating amounts
CC   of VEGF-D can be used to treat anhydrotic ectodermal dysplasia. VEGF-D
CC   antibodies are useful for detecting tumours expressing VEGF-D. Fully-
CC   processed VEGF-D can be used to stimulate at least one VEGF-D bioactivity
CC   chosen from endothelial cell proliferation, migration, survival and
CC   differentiation and lymphangiogenesis without inducing vascular
CC   permeability
XX
SQ   Sequence 109 AA;
XX
Query Match   80.0%;   Score 80;   DB 2;   Length 109;
Best Local Similarity   93.8%;   Pred. No. 0.00036;
Matches 15;   Conservative   0; Mismatches   1;   Indels   0;   Gaps   0;

Qy   2 ASELGKSTNTFCKPPC 17
         ||||||||||| ||||
Db   29 ASELGKSTNTFFKPPC 44

RESULT 11
AAB11931
ID   AAB11931 standard; protein; 109 AA.
XX
AC   AAB11931;
XX
DT   20-NOV-2000 (first entry)
XX
DE   Human truncated VEGF-D.
XX
KW   Truncated VEGF-D; vascular endothelial growth factor; human;
KW   monoclonal antibody; VEGF receptor; VEGFR-2; VEGFR-3;
KW   vascular permeability disorder; endothelial cell proliferative disorder;
KW   angiogenic disorder; lymphangiogenic disorder;
KW   neovascularisation disorder; endothelial cell differentiation disorder;
KW   cancer; diabetic retinopathy; psoriasis; arthropathy; pulmonary oedema;
KW   detection; diagnosis; imaging; lymphatic vasculature.
XX
OS   Homo sapiens.
XX
PN   WO200037025-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US031332.
XX
PR   21-DEC-1998;   98US-0113254P.
PR   17-MAY-1999;   99US-0134556P.

XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Stacker SA;
XX
DR   WPI; 2000-442498/38.
XX
PT   Novel compositions comprising antibodies reactive to vascular endothelial
PT   growth factor-D, useful for treating, e.g. angiogenesis, lymphogiogenesis
PT   and neovascularization disorders.
XX
PS   Claim 1; Fig 1; 44pp; English.
XX
CC   This sequence represents a 109 amino acid truncated human VEGF-D
CC   (vascular endothelial growth factor D), lacking both the N- and C-
CC   terminal regions. The invention relates to a monoclonal antibody, or
CC   fragments thereof, which is specifically reactive with the truncated
CC   human VEGF-D, and methods of preparing the antibody. The antibody of the
CC   invention interferes with the binding of VEGF-D to the VEGF receptors
CC   VEGFR-2 and VEGFR-3, but does not interfere with the binding of VEGF to
CC   these receptors and additionally is not reactive with VEGF-C. The
CC   antibody may be used to treat disorders associated with vascular
CC   permeability, endothelial cell proliferation, angiogenesis,
CC   lymphangiogenesis, neovascularisation and endothelial cell
CC   differentiation, especially cancer, diabetic retinopathy, psoriasis, and
CC   arthropathies. The antibody may also be used to treat fluid accumulation
CC   in the heart and/or lung via modulation of vascular permeability. It may
CC   additionally be used to detect VEGF-D and may be used to image lymphatic
CC   vasculature in tissue
XX
SQ   Sequence 109 AA;

Query Match   80.0%;   Score 80;   DB 3;   Length 109;
Best Local Similarity   93.8%;   Pred. No. 0.00036;
Matches 15;   Conservative   0; Mismatches   1;   Indels   1;   Gaps   0;

Qy   2 ASELGKSTNTFCKPPC 17
         ||||||||||| ||||
Db   29 ASELGKSTNTFFKPPC 44

RESULT 12
ABB84621
ID   ABB84621 standard; protein; 109 AA.
XX
AC   ABB84621;
XX
DT   01-APR-2003 (first entry)
XX
DE   Human wild-type VEGF-D monomer SEQ ID 3.
XX
KW   Human; single-chain; extracellular ligand-binding domain; VEGF;
KW   vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
KW   VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
KW   lymphangiogenesis.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Region   8..18
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"
FT   Region   36..49
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"
FT   Region   55..60
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"
FT   Misc-difference 60
FT   /note= "This residues is described as Gln in Claim 9"
FT   Region   70..86
FT   /note= "region of monomer likely to be modified by
FT   mutation as described in claim 9"

```
XX
PN   WO200281520-A2.
XX
PD   17-OCT-2002.
XX
PF   08-APR-2002; 2002WO-DK000233.
XX
PR   06-APR-2001; 2001DK-00000578.
PR   06-APR-2001; 2001US-0282239P.
XX
PA   (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI   Boesen TP, Halkier T;
XX
DR   WPI; 2003-058505/05.
XX
PT   Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds
PT   to extracellular ligand-binding domain of vascular endothelial growth
PT   factor type 2/type 3 receptor but does not activate the receptor.
XX
PS   Claim 9; Page 66; 71pp; English.
XX
CC   This invention describes a novel single-chain dimeric polypeptide which
CC   binds to extracellular ligand-binding domain of vascular endothelial
CC   growth factor (VEGF) type 2 receptor (KDR) or VEGF type 3 receptor (Flt-
CC   4). The polypeptide of the invention comprises two receptor-binding sites
CC   of which one is capable of binding to a ligand-binding domain of the
CC   receptor and one is incapable of effectively binding to a ligand-binding
CC   domain of the receptor, and at least one monomer of the dimeric
CC   polypeptide is derived from VEGF, VEGF-C or VEGF-D, where the polypeptide
CC   is capable of binding to the receptor, but incapable of activating the
CC   receptor. The polypeptide of the invention is useful for preparing a
CC   medicament for preventing or treating a disease or condition involving
CC   increased signal transduction from, or an increased activation of a VEGF
CC   type 2 or type 3 receptor e.g. for inhibiting angiogenesis or
CC   lymphangiogenesis. This sequence represents a human single-chain VEGF-D
CC   monomer which can be modified and used in the construction of a VEGF-
CC   based KDR antagonist described in the disclosure of the invention
XX
SQ   Sequence 109 AA;

Query Match         80.0%;    Score 80;   DB 6;   Length 109;
Best Local Similarity   93.8%;    Pred. No. 0.00036;
Matches   15;   Conservative    0;   Mismatches    0;   Indels   1;   Gaps   0;

Qy    2 ASELGKSTNTFCKPPC 17
          |||||||||| |||
Db   29 ASELGKSTNTFFKPPC 44

RESULT 13
ABG73750
ID   ABG73750 standard; protein; 109 AA.
XX
AC   ABG73750;
XX
DT   01-APR-2003  (first entry)
XX
DE   Human VEGF-D monomer unit E57R variant.
XX
KW   Human; single-chain; extracellular ligand-binding domain; VEGF;
KW   vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
KW   VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
KW   lymphangiogenesis; mutant; mutein; variant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Misc-difference 10
FT                  /note= "This wild-type residue is replaced by Arg or Glu
FT                  in the first monomer unit of the VEGF-D dimer if the E57R
FT                  mutation has not occurred (see Claim 16) and is
FT                  optionally replaced if the E57R mutation has occurred.
FT                  The claim describes this residue as Ser but is shown as
FT                  Ile in the sequence listing"
FT   Misc-difference 37
FT                  /note= "This wild-type Asn residue is optionally replaced
FT                  by Arg in the second monomer unit of the VEGF-D dimer
FT                  (See Claim 11)"
FT   Misc-difference 38
FT                  /note= "This wild type Thr residue is optionally replaced
FT                  by Arg or Glu in the second monomer unit of the VEGF-D
FT                  dimer (see Claims 11 and 16)"
FT   Misc-difference 39
FT                  /note= "This wild type Phe residue is optionally replaced
FT                  by Arg or Glu in the second monomer unit of the VEGF-D
FT                  dimer (see Claims 11 and 16)"
FT   Misc-difference 40
FT                  /note= "This wild type Phe residue is optionally replaced
FT                  by Arg in the second monomer unit of the VEGF-D dimer
FT                  (see Claim 11)"
FT   Misc-difference 57
FT                  /label= E57R
FT                  /note= "Wild type Gln is replaced by Arg in the first
FT                  monomer unit of the VEGF-D dimer (See Claim 11) and is
FT                  optionally replaced if the S10R/E mutation has occurred
FT                  (see Claim 16)"
FT   Misc-difference 76
FT                  /note= "This wild type Ile residue is optionally replaced
FT                  by Arg or Glu in the second monomer unit of the VEGF-D
FT                  dimer (see Claim 16)"
XX
PN   WO200281520-A2.
XX
PD   17-OCT-2002.
XX
PF   08-APR-2002; 2002WO-DK000233.
XX
PR   06-APR-2001; 2001DK-00000578.
PR   06-APR-2001; 2001US-0282239P.
XX
PA   (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI   Boesen TP, Halkier T;
XX
DR   WPI; 2003-058505/05.
XX
PT   Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds
PT   to extracellular ligand-binding domain of vascular endothelial growth
PT   factor type 2/type 3 receptor but does not activate the receptor.
XX
PS   Claim 11; Page; 71pp; English.
XX
CC   This invention describes a novel single-chain dimeric polypeptide which
CC   binds to extracellular ligand-binding domain of vascular endothelial
CC   growth factor (VEGF) type 2 receptor (KDR) or VEGF type 3 receptor (Flt-
CC   4). The polypeptide of the invention comprises two receptor-binding sites
CC   of which one is capable of binding to a ligand-binding domain of the
CC   receptor and one is incapable of effectively binding to a ligand-binding
CC   domain of the receptor, and at least one monomer of the dimeric
CC   polypeptide is derived from VEGF, VEGF-C or VEGF-D, where the polypeptide
CC   is capable of binding to the receptor, but incapable of activating the
CC   receptor. The polypeptide of the invention is useful for preparing a
CC   medicament for preventing or treating a disease or condition involving
CC   increased signal transduction from, or an increased activation of a VEGF
CC   type 2 or type 3 receptor e.g. for inhibiting angiogenesis or
CC   lymphangiogenesis. This sequence represents a variant of the human VEGF-D
CC   monomer unit used in the construction of a VEGF-D dimer described in the
CC   disclosure of the invention. In one instance a polypeptide is claimed
CC   comprising a first monomer derived from VEGF-D having at least the
CC   mutation E57R and optionally comprising a second monomer derived from
CC   VEGF-D having at least one mutation selected from the group consisting of
CC   N37R, T38T, F39R and F40R. In a second instance a polypeptide is claimed
CC   comprising a first monomer containing a substitution consisting of S10R,
CC   S10E and E57R (although the residue at position 10 is an Ile), and/or in
```

CC   the other VEGF-D derived monomer at least one substitution selected from
CC   the group consisting of T38R, T38E, F39E, F39R, I76R and I76E. NOTE: This
CC   sequence is not represented in the body of the specification but has been
CC   constructed from the wild-type VEGF-D sequence represented in ABB4621
XX
SQ   Sequence 109 AA;

Query Match   80.0%; Score 80; DB 6; Length 109;
Best Local Similarity   93.8%; Pred. No. 0.00036;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   2 ASELGKSTNTFCKPPC 17
            |||||||||| ||||
Db   29 ASELGKSTNTFFKPPC 44

RESULT 14
ABG73779
ID   ABG73779 standard; protein; 287 AA.
XX
AC   ABG73779;
XX
DT   03-APR-2003 (first entry)
XX
DE   Human NVR protein.
XX
KW   NVR; human; endothelial growth factor; cytostatic; cancer; angiogenesis;
KW   cell proliferation; revascularisation; amputation; vasculogenesis;
KW   transplant; brain; breast; intestine; kidney; lung; ovary; pancreas;
KW   prostate; uterus; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Misc-difference 281
FT   /note= "Encoded by TAA, an in frame stop codon which
FT   interrupts the coding region as shown in Figure 1A-B.
FT   This site is the end of the protein sequence represented
FT   in SEQ ID 1 of the Sequence listing"
FT   Region   282..287
FT   /note= "Region not represented in SEQ ID 1 of the
FT   Sequence listing"
XX
PN   US2002155538-A1.
XX
PD   24-OCT-2002.
XX
PF   09-JAN-2002; 2002US-00044622.
XX
PR   23-JAN-1997; 97US-00788812.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Bandman O, Goli SK, Murry LE;
XX
DR   WPI; 2003-182635/18.
DR   N-PSDB; ABQ77105.
XX
PT   New endothelial growth factor polypeptide and polynucleotides, useful for
PT   diagnosing, preventing, and treating cancer and other conditions or
PT   diseases involving angiogenesis and cell proliferation.
XX
PS   Claim 1; Fig 1A-B; 28pp; English.
XX
CC   This invention describes a novel human endothelial growth factor
CC   polypeptide which has cytostatic activity. The polypeptide and its
CC   encoding polynucleotide are useful in the diagnosis, prevention, and
CC   treatment of cancer and other conditions or diseases involving
CC   angiogenesis and cell proliferation. NVR may also be used to promote
CC   revascularisation following traumatic amputation and surgical
CC   reconstruction or added to a tissue culture to promote vasculogenesis in
CC   tissues for autologous or heterologous transplant. Antagonists or
CC   inhibitors of NVR may be used to suppress or prevent angiogenesis and

CC   thus prevent the growth and development of cancers such as cancer of the
CC   brain, breast, intestine, kidney, lung, ovary, pancreas, prostate or
CC   uterus. The products of the invention can be used for gene therapy. This
CC   sequence represents the human NVR protein described in the disclosure of
CC   the invention
XX
SQ   Sequence 287 AA;

Query Match   80.0%; Score 80; DB 6; Length 287;
Best Local Similarity   93.8%; Pred. No. 0.0009;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   2 ASELGKSTNTFCKPPC 17
            |||||||||| ||||
Db   121 ASELGKSTNTFFKPPC 136

RESULT 15
AAW53240
ID   AAW53240 standard; protein; 325 AA.
XX
AC   AAW53240;
XX
DT   03-AUG-1998 (first entry)
XX
DE   Homo sapiens vascular endothelial growth factor D (VEGF-D).
XX
KW   vascular endothelial growth factor; VEGF-D; angiogenesis; modification;
KW   acceleration; wound healing; tissue; organ; transplants;
KW   collateral circulation; infarction; arterial stenosis;
KW   coronary artery disease; inhibition; cancer; treatment;
KW   diabetic retinopathy; lung disorders; blood circulation;
KW   gaseous exchange; chronic obstructive airway disease;
KW   intestinal malabsorptive syndrome; biopsy; metastatic risk; detection;
KW   diagnosis; congestive heart failure.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Region   126..128
FT   /note= "potential N-linked glycosylation site"
FT   Region   156..158
FT   /note= "potential N-linked glycosylation site"
FT   Region   258..260
FT   /note= "potential N-linked glycosylation site"
XX
PN   WO9807832-A1.
XX
PD   26-FEB-1998.
XX
PF   21-AUG-1997; 97WO-US014696.
XX
PR   23-AUG-1996; 96AU-00001825.
PR   23-AUG-1996; 96US-0023751P.
PR   11-NOV-1996; 96AU-0003554.
PR   14-NOV-1996; 96US-0031097P.
PR   05-FEB-1997; 97AU-00004954.
PR   10-FEB-1997; 97US-0038814P.
PR   19-JUN-1997; 97AU-00007435.
PR   01-JUL-1997; 97US-0051426P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
PI   Achen MG, Wilks AF, Stacker SA, Alitalo K;
XX
DR   WPI; 1998-179057/16.
DR   N-PSDB; AAV20806.
XX
PT   New isolated vascular endothelial growth factor-D - used to develop
PT   products for use in e.g. modifying angiogenesis or treating lung, heart
PT   or intestinal disorders.
XX

PS   Claim 16; Page 57-58; 101pp; English.
XX
CC   The sequence is that of human breast vascular endothelial growth factor D
CC   (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in
CC   wound healing, tissue or organ transplantation, or to establish
CC   collateral circulation in tissue infarction or arterial stenosis, such as
CC   coronary artery disease, and inhibition of angiogenesis in the treatment
CC   of cancer or of diabetic retinopathy. It can also be used in the
CC   treatment of lung disorders to improve blood circulation in the lung
CC   and/or gaseous exchange between the lungs and the blood stream or to
CC   improve blood circulation to the heart and O2 gas permeability in cases
CC   of cardiac insufficiency, to improve blood flow and gaseous exchange in
CC   chronic obstructive airway disease, or to treat malabsorptive syndromes
CC   in the intestinal tract. Quantitation of VEGF-D in cancer biopsy
CC   specimens may be useful as an indicator of future metastatic risk.
CC   Antagonists can be used for treating e.g. conditions such as congestive
CC   heart failure, involving accumulations of fluid in the lung resulting
CC   from increases in vascular permeability. The products can also be used
CC   for detection and diagnosis
XX
SQ   Sequence 325 AA;

Query Match   80.0%;   Score 80; DB 2;   Length 325;
Best Local Similarity   93.8%;   Pred. No. 0.001;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   2 ASELGKSTNTFCKPPC 17
          |||||||||| ||||
Db   92 ASELGKSTNTFFKPPC 107

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OM protein - protein search, using sw model

Run on:      September 5, 2004, 10:00:15 ; Search time 47.7374 Seconds
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Searched:        1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters:   1298764

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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             9:  /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	100	100.0	17	9	US-09-761-636A-8	Sequence 8, Appli
2	97	97.0	17	9	US-09-761-636A-27	Sequence 27, Appl
3	97	97.0	17	9	US-09-761-636A-31	Sequence 31, Appl
4	93	93.0	17	9	US-09-761-636A-28	Sequence 28, Appl
5	93	93.0	17	9	US-09-761-636A-30	Sequence 30, Appl
6	93	93.0	17	9	US-09-761-636A-32	Sequence 32, Appl
7	89	89.0	17	9	US-09-761-636A-29	Sequence 29, Appli
8	80	80.0	73	9	US-09-761-636A-3	Sequence 3, Appli
9	80	80.0	96	9	US-09-761-636A-1	Sequence 1, Appli
10	80	80.0	109	9	US-09-956-095-3	Sequence 3, Appli
11	80	80.0	109	9	US-09-219-345A-1	Sequence 1, Appli
12	80	80.0	109	16	US-10-779-731-1	Sequence 1, Appli
13	80	80.0	197	12	US-10-352-153-8	Sequence 8, Appli
14	80	80.0	280	13	US-10-044-622-1	Sequence 1, Appli
15	80	80.0	325	14	US-10-274-953-3	Sequence 3, Appli
16	80	80.0	325	14	US-10-161-694-3	Sequence 3, Appli
17	80	80.0	354	9	US-09-956-095-2	Sequence 2, Appli
18	80	80.0	354	9	US-09-219-345A-11	Sequence 11, Appl
19	80	80.0	354	9	US-09-795-006A-119	Sequence 119, App
20	80	80.0	354	10	US-09-375-248-6	Sequence 6, Appli
21	80	80.0	354	12	US-09-765-534B-22	Sequence 22, Appl
22	80	80.0	354	12	US-10-661-740-6	Sequence 6, Appl
23	80	80.0	354	14	US-10-262-538-26	Sequence 26, Appl
24	80	80.0	354	14	US-10-274-953-5	Sequence 5, Appli
25	80	80.0	354	14	US-10-161-694-5	Sequence 5, Appli
26	80	80.0	354	14	US-10-174-930-1	Sequence 1, Appli
27	80	80.0	362	13	US-10-139-876-4	Sequence 4, Appli
28	77	77.0	48	13	US-10-139-876-5	Sequence 5, Appli
29	77	77.0	81	13	US-10-086-623-18	Sequence 18, Appl
30	77	77.0	81	14	US-10-260-539-18	Sequence 18, Appl
31	77	77.0	110	10	US-09-847-524-6	Sequence 6, Appli
32	77	77.0	321	10	US-09-847-524-4	Sequence 4, Appli
33	77	77.0	321	14	US-10-274-953-9	Sequence 9, Appli
34	77	77.0	321	14	US-10-161-694-9	Sequence 9, Appli
35	77	77.0	358	9	US-09-852-209A-13	Sequence 13, Appl
36	77	77.0	358	10	US-09-847-524-2	Sequence 2, Appli
37	77	77.0	358	12	US-10-439-337A-13	Sequence 13, Appl
38	77	77.0	358	12	US-10-303-997B-13	Sequence 13, Appl
39	77	77.0	358	13	US-10-139-876-2	Sequence 2, Appli
40	77	77.0	358	14	US-10-131-600-13	Sequence 13, Appl
41	77	77.0	358	14	US-10-274-953-8	Sequence 8, Appli
42	77	77.0	358	14	US-10-161-694-8	Sequence 8, Appli
43	72	72.0	13	9	US-09-761-636A-5	Sequence 5, Appli
44	69	69.0	13	9	US-09-761-636A-15	Sequence 15, Appli
45	65	65.0	13	9	US-09-761-636A-16	Sequence 16, Appl

ALIGNMENTS

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RESULT 1
US-09-761-636A-8
; Sequence 8, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-8

  Query Match             100.0%;  Score 100;  DB 9;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CASELGKSTNTFCKPPC 17
              |||||||||||||||||
Db          1 CASELGKSTNTFCKPPC 17

RESULT 2
US-09-761-636A-27
; Sequence 27, Application US/09761636A
; Patent No. US20020065218A1
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; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: synthetic construct
US-09-761-636A-27

Query Match          97.0%;  Score 97;  DB 9;  Length 17;
Best Local Similarity 94.1%;  Pred. No. 9.2e-08;
Matches   16;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy          1 CASELGKSTNTFCKPPC 17
                ||:||||||||||||||
Db          1 CATELGKSTNTFCKPPC 17


RESULT 3
US-09-761-636A-31
; Sequence 31, Application US/09761636A
; Patent No. US2002065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: synthetic construct
US-09-761-636A-31

Query Match          97.0%;  Score 97;  DB 9;  Length 17;
Best Local Similarity 94.1%;  Pred. No. 9.2e-08;
Matches   16;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy          1 CASELGKSTNTFCKPPC 17
                ||:||||||||||||||
Db          1 CATELGKSTNTYCKPPC 17


RESULT 4
US-09-761-636A-28
; Sequence 28, Application US/09761636A
; Patent No. US2002065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
```

```
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: synthetic construct
US-09-761-636A-28

Query Match          93.0%;  Score 93;  DB 9;  Length 17;
Best Local Similarity 88.2%;  Pred. No. 3.7e-07;
Matches   15;  Conservative   2;  Mismatches   2;  Indels   0;  Gaps   0;

Qy          1 CASELGKSTNTFCKPPC 17
                |||||||::||||||||
Db          1 CASELGKTSNTFCKPPC 17


RESULT 5
US-09-761-636A-30
; Sequence 30, Application US/09761636A
; Patent No. US2002065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: synthetic construct
US-09-761-636A-30

Query Match          93.0%;  Score 93;  DB 9;  Length 17;
Best Local Similarity 88.2%;  Pred. No. 3.7e-07;
Matches   15;  Conservative   2;  Mismatches   2;  Indels   0;  Gaps   0;

Qy          1 CASELGKSTNTFCKPPC 17
                ||||||||:||||||||
Db          1 CASELGRSTNSFCKPPC 17


RESULT 6
US-09-761-636A-32
; Sequence 32, Application US/09761636A
; Patent No. US2002065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
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; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-32

Query Match　　　　93.0%;　　Score 93;　DB 9;　Length 17;
Best Local Similarity　88.2%;　Pred. No. 3.7e-07;
Matches　15;　Conservative　2;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　1 CASELGKSTNTFCKPPC 17
　　　 ||||||:||||||:|||||
Db　1 CASELGRSTNSFCKPPC 17

RESULT 7
US-09-761-636A-29
; Sequence 29, Application US/09761636A
; Patent No. US2002006521Al
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-29

Query Match　　　　89.0%;　　Score 89;　DB 9;　Length 17;
Best Local Similarity　82.4%;　Pred. No. 1.5e-06;
Matches　14;　Conservative　3;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　1 CASELGKSTNTFCKPPC 17
　　　 |||:||||||:|:|||||
Db　1 CASDVGKSTNTWCKPPC 17

RESULT 8
US-09-761-636A-3
; Sequence 3, Application US/09761636A
; Patent No. US2002006521Al
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid residues Val101-Thr173 of VEGF-D
US-09-761-636A-3

Query Match　　　　80.0%;　　Score 80;　DB 9;　Length 73;
Best Local Similarity　93.8%;　Pred. No. 0.00014;
Matches　15;　Conservative　0;　Mismatches　1;　Indels　0;　Gaps　0;

Qy　2 ASELGKSTNTFCKPPC 17
　　　 |||||||||| |||
Db 21 ASELGKSTNTFFKPPC 36

RESULT 9
US-09-761-636A-1
; Sequence 1, Application US/09761636A
; Patent No. US2002006521A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid residues of Val101-Pro196 of VEGF-D
US-09-761-636A-1

Query Match　　　　80.0%;　　Score 80;　DB 9;　Length 96;
Best Local Similarity　93.8%;　Pred. No. 0.00018;
Matches　15;　Conservative　0;　Mismatches　1;　Indels　0;　Gaps　0;

Qy　2 ASELGKSTNTFCKPPC 17
　　　 |||||||||| |||
Db 21 ASELGKSTNTFFKPPC 36

RESULT 10
US-09-956-095-3
; Sequence 3, Application US/09956095
; Patent No. US20020102260A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steven A.
; TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
; TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
; TITLE OF INVENTION: VASCULARIZATION OF TISSUE
; FILE REFERENCE: 1064/48666PC
; CURRENT APPLICATION NUMBER: US/09/956,095
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 09/796,714
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/234,196
; PRIOR FILING DATE: 2000-09-20

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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-095-3

Query Match        80.0%;  Score 80;  DB 9;  Length 109;
Best Local Similarity   93.8%;  Pred. No. 0.00021;
Matches  15;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy         2 ASELGKSTNTFCKPPC 17
             ||||||||||| ||||
Db        29 ASELGKSTNTFFKPPC 44


RESULT 11
US-09-219-345A-1
; Sequence 1, Application US/09219345A
; Patent No. US2002012722A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; TITLE OF INVENTION: EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING
; TITLE OF INVENTION: MELANOMAS
; FILE REFERENCE: 1064/44385 Marc ACHEN
; CURRENT APPLICATION NUMBER: US/09/219,345A
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: AU PP 1131
; PRIOR FILING DATE: 1997-12-24
; PRIOR APPLICATION NUMBER: US 60/087,392
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-219-345A-1

Query Match        80.0%;  Score 80;  DB 9;  Length 109;
Best Local Similarity   93.8%;  Pred. No. 0.00021;
Matches  15;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy         2 ASELGKSTNTFCKPPC 17
             ||||||||||| ||||
Db        29 ASELGKSTNTFFKPPC 44


RESULT 12
US-10-779-731-1
; Sequence 1, Application US/10779731
; Publication No. US2004141917A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/10/779,731
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US/10/100,037
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/469,186
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113,254
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/134,556
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 109
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-779-731-1

Query Match        80.0%;  Score 80;  DB 16;  Length 109;
Best Local Similarity   93.8%;  Pred. No. 0.00021;
Matches  15;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy         2 ASELGKSTNTFCKPPC 17
             ||||||||||| ||||
Db        29 ASELGKSTNTFFKPPC 44


RESULT 13
US-10-352-153-8
; Sequence 8, Application US/10352153
; Publication No. US2003021101A1
; GENERAL INFORMATION:
; APPLICANT: Wise, Lyn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stacker, Stephen
; TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
; TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
; TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence Listing for 09/431,833
; CURRENT APPLICATION NUMBER: US/10/352,153
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US/09/431,888A
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,689
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,800
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-352-153-8

Query Match        80.0%;  Score 80;  DB 12;  Length 197;
Best Local Similarity   93.8%;  Pred. No. 0.00036;
Matches  15;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy         2 ASELGKSTNTFCKPPC 17
             ||||||||||| ||||
Db        45 ASELGKSTNTFFKPPC 60


RESULT 14
US-10-044-622-1
; Sequence 1, Application US/10044622
; Publication No. US2002015538A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
;            Goli, Surya K.
;            Murry, Lynn E.
; TITLE OF INVENTION: NOVEL ENDOTHELIAL GROWTH
;                     FACTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Incyte Pharmaceuticals, Inc.
;      STREET: 3174 Porter Drive
;      CITY: Palo Alto
;      STATE: CA
;      COUNTRY: USA
;      ZIP: 94304
; COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
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```
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 628-8800
;       TELEFAX:    (202) 628-8844
;       TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  325 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
;     ORIGINAL SOURCE:
;       TISSUE TYPE:  Human Breast
US-10-274-953-3

Query Match             80.0%;  Score 80;  DB 14;  Length 325;
Best Local Similarity   93.8%;  Pred. No. 0.00059;
Matches  15;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy      2 ASELGKSTNTFCKPPC 17
          |||||||||| ||||
Db     92 ASELGKSTNTFFKPPC 107

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;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/044,622
;     FILING DATE: 09-Jan-2002
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/788,812
;     FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Billings, Lucy J.
;     REGISTRATION NUMBER: 36,749
;     REFERENCE/DOCKET NUMBER: PP-0185 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-855-0555
;     TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 280 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     IMMEDIATE SOURCE:
;       LIBRARY: LUNGAST01
;       CLONE: 873352
;     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-622-1

Query Match             80.0%;  Score 80;  DB 13;  Length 280;
Best Local Similarity   93.8%;  Pred. No. 0.00051;
Matches  15;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy      2 ASELGKSTNTFCKPPC 17
          |||||||||| ||||
Db    121 ASELGKSTNTFFKPPC 136


RESULT 15
US-10-274-953-3
; Sequence 3, Application US/10274953
; Publication No. US20030114658A1
; GENERAL INFORMATION:
;   APPLICANT: Marc G. ACHEN
;   APPLICANT: Andrew F. WILKS
;   APPLICANT: Steven A. STACKER
;   APPLICANT: Kari ALITALO
;   TITLE OF INVENTION: GROWTH FACTOR
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;     STREET: 1200 G Street, NW, Suite 700
;     CITY: Washington
;     STATE: DC
;     COUNTRY: United States of America
;     ZIP: 20005
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/274,953
;     FILING DATE: 22-oct-2002
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/296,275
;     FILING DATE:
;     APPLICATION NUMBER: 08/915,795
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: EVANS, Joseph D.
;     REGISTRATION NUMBER: 26,269
;     REFERENCE/DOCKET NUMBER: 1064/42983
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            GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:    September 5, 2004, 09:55:30 ; Search time 15.1111 Seconds
                                          (without alignments)
                                          58.079 Million cell updates/sec

Title:          US-09-761-636A-8
Perfect score:  100
Sequence:       1 CASELGKSTNTFCKPPC 17

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                Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters:     389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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    2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
    3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
    4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
    5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
    6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	80	80.0	109	4	US-09-469-186-1	Sequence 1, Appli
2	80	80.0	109	4	US-09-469-185-1	Sequence 1, Appli
3	80	80.0	197	4	US-08-431-888-8	Sequence 8, Appli
4	80	80.0	325	3	US-08-915-795-3	Sequence 3, Appli
5	80	80.0	354	3	US-08-915-795-5	Sequence 5, Appli
6	77	77.0	321	3	US-08-915-795-9	Sequence 9, Appli
7	77	77.0	358	3	US-08-915-795-8	Sequence 8, Appli
8	59	59.0	415	4	US-08-795-430-11	Sequence 11, Appli
9	59	59.0	415	4	US-09-355-700-11	Sequence 11, Appli
10	59	59.0	415	4	US-08-601-132-41	Sequence 41, Appli
11	59	59.0	415	4	US-08-671-573B-41	Sequence 41, Appli
12	59	59.0	418	3	US-08-795-430-13	Sequence 13, Appli
13	59	59.0	418	4	US-09-355-700-13	Sequence 13, Appli
14	58	58.0	160	4	US-09-431-888-7	Sequence 59, Appli
15	58	58.0	228	4	US-08-999-811-4	Sequence 7, Appli
16	58	58.0	350	2	US-08-824-996-2	Sequence 4, Appli
17	58	58.0	350	3	US-09-042-105-4	Sequence 2, Appli
18	58	58.0	350	3	US-08-510-133A-33	Sequence 33, Appli
19	58	58.0	350	3	US-08-585-895-33	Sequence 33, Appli
20	58	58.0	350	2	US-08-999-811-2	Sequence 2, Appli
21	58	58.0	419	3	US-09-042-105-2	Sequence 2, Appli
22	58	58.0	419	3	US-09-042-105-18	Sequence 18, Appli
23	58	58.0	419	3	US-08-795-430-8	Sequence 8, Appli
24	58	58.0	419	3	US-08-510-133A-35	Sequence 35, Appli
25	58	58.0	419	3	US-09-355-700-8	Sequence 8, Appli
26	58	58.0	419	4	US-08-601-132-33	Sequence 33, Appli
28	58	58.0	419	4	US-08-706-054A-3	Sequence 3, Appli
29	58	58.0	419	4	US-09-313-299-3	Sequence 3, Appli
30	58	58.0	419	4	US-08-465-968-2	Sequence 2, Appli
31	58	58.0	419	4	US-08-671-573B-33	Sequence 33, Appl
32	49	49.0	419	5	PCT-US96-09001-2	Sequence 2, Appli
33	47	47.0	120	2	US-09-355-700-58	Sequence 58, Appl
34	47	47.0	120	4	US-08-938-975-2	Sequence 2, Appli
35	47	47.0	120	4	US-09-321-399-2	Sequence 2, Appli
36	46	46.0	128	4	US-09-322-379-2	Sequence 2, Appli
37	46	46.0	128	4	US-09-328-352-4400	Sequence 4400, Ap
38	46	46.0	260	4	US-09-162-021B-4	Sequence 4, Appli
39	45	45.0	20	3	US-09-230-222-28	Sequence 28, Appl
40	45	45.0	21	4	US-09-230-225B-9	Sequence 9, Appli
41	43	43.0	83	3	US-08-875-811-2	Sequence 2, Appli
42	43	43.0	83	4	US-09-071-672-3	Sequence 3, Appli
43	43	43.0	83	3	US-09-986-119-3	Sequence 3, Appli
44	43	43.0	104	1	US-08-283-971-1	Sequence 1, Appli
45	43	43.0	104	1	US-07-921-619-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-09-469-186-1
; Sequence 1, Application US/09469186
; Patent No. 6383484
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,186
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-186-1

Query Match            80.0%;  Score 80;  DB 4;  Length 109;
Best Local Similarity  93.8%;  Pred. No. 5e-05;
Matches  15;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    2 ASELGKSTNTFCKPPC 17
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Db   29 ASELGKSTNTFFKPPC 44

RESULT 2
US-09-469-185-1
; Sequence 1, Application US/09469185
; Patent No. 6531185
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,185
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
US-09-469-186-1
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;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-469-185-1

Query Match          80.0%;   Score 80;  DB 4;  Length 109;
Best Local Similarity 93.8%;   Pred. No. 5e-05;
Matches   15;   Conservative   0;  Mismatches   1;  Indels   1;  Gaps   0;

Qy        2  ASELGKSTNTFCKPPC 17
             ||||||||||||| ||||
Db       29  ASELGKSTNTFFKPPC 44


RESULT 3
US-09-431-888-8
;  Sequence 8, Application US/09431888A
;  Patent No. 6541008
;  GENERAL INFORMATION:
;  APPLICANT: Wise, Lyn M
;  APPLICANT: Mercer, Andrew A
;  APPLICANT: Savory, Loreen J
;  APPLICANT: Fleming, Stephen B
;  APPLICANT: Stacker, Stephen
;  TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
;  TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
;  TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
;  FILE REFERENCE: Sequence Listing for 09/431,833
;  Patent No. 6541008
;  CURRENT APPLICATION NUMBER: US/09/431,888A
;  CURRENT FILING DATE: 1999-11-02
;  EARLIER APPLICATION NUMBER: 60/106,689
;  EARLIER FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: 60/106,800
;  EARLIER FILING DATE: 1998-11-03
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 8
;   TYPE: PRT
;   LENGTH: 197
;   ORGANISM: Homo sapiens
US-09-431-888-8

Query Match          80.0%;   Score 80;  DB 4;  Length 197;
Best Local Similarity 93.8%;   Pred. No. 9.1e-05;
Matches   15;   Conservative   0;  Mismatches   1;  Indels   1;  Gaps   0;

Qy        2  ASELGKSTNTFCKPPC 17
             ||||||||||||| ||||
Db       45  ASELGKSTNTFFKPPC 60


RESULT 4
US-08-915-795-3
;  Sequence 3, Application US/08915795
;  Patent No. 6235713
;  GENERAL INFORMATION:
;  APPLICANT: Marc G. ACHEN
;  APPLICANT: Andrew F. WILKS
;  APPLICANT: Steven A. STACKER
;  APPLICANT: Kari ALITALO
;  TITLE OF INVENTION: GROWTH FACTOR
;  NUMBER OF SEQUENCES: 11
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;   STREET: 1200 G Street, NW, Suite 700
;   CITY: Washington
;   STATE: DC
;   COUNTRY: United States of America
;   ZIP: 20005
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
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;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/915,795
;   FILING DATE:
;   CLASSIFICATION: 536
;  ATTORNEY/AGENT INFORMATION:
;   NAME: EVANS, Joseph D.
;   REGISTRATION NUMBER: 26,269
;   REFERENCE/DOCKET NUMBER: 1064/42983
;  TELECOMUNICATION INFORMATION:
;   TELEPHONE: (202) 628-8800
;   TELEFAX:   (202) 628-8844
;   TELEX: N/A
;  INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 325 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ORIGINAL SOURCE:
;   TISSUE TYPE: Human Breast
;  US-08-915-795-3

Query Match          80.0%;   Score 80;  DB 3;  Length 325;
Best Local Similarity 93.8%;   Pred. No. 0.00015;
Matches   15;   Conservative   0;  Mismatches   1;  Indels   1;  Gaps   0;

Qy        2  ASELGKSTNTFCKPPC 17
             ||||||||||||| ||||
Db       92  ASELGKSTNTFFKPPC 107


RESULT 5
US-08-915-795-5
;  Sequence 5, Application US/08915795
;  Patent No. 6235713
;  GENERAL INFORMATION:
;  APPLICANT: Marc G. ACHEN
;  APPLICANT: Andrew F. WILKS
;  APPLICANT: Steven A. STACKER
;  APPLICANT: Kari ALITALO
;  TITLE OF INVENTION: GROWTH FACTOR
;  NUMBER OF SEQUENCES: 11
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;   STREET: 1200 G Street, NW, Suite 700
;   CITY: Washington
;   STATE: DC
;   COUNTRY: United States of America
;   ZIP: 20005
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/915,795
;   FILING DATE:
;   CLASSIFICATION: 536
;  ATTORNEY/AGENT INFORMATION:
;   NAME: EVANS, Joseph D.
;   REGISTRATION NUMBER: 26,269
;   REFERENCE/DOCKET NUMBER: 1064/42983
;  TELECOMUNICATION INFORMATION:
;   TELEPHONE: (202) 628-8800
;   TELEFAX:   (202) 628-8844
;   TELEX: N/A
;  INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 354 amino acids
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;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ORIGINAL SOURCE:
;   TISSUE TYPE: Human Lung
US-08-915-795-5

Query Match   80.0%; Score 80; DB 3; Length 354;
Best Local Similarity   93.8%; Pred. No. 0.00016;
Matches 15; Conservative   0; Mismatches 1; Indels 0; Gaps 0;

Qy   2 ASELGKSTNTFCKPPC 17
          |||||||||||| ||||
Db   121 ASELGKSTNTFFKPPC 136

RESULT 6
US-08-915-795-9
; Sequence 9, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
;   APPLICANT: Marc G. ACHEN
;   APPLICANT: Andrew F. WILKS
;   APPLICANT: Steven A. STACKER
;   APPLICANT: Kari ALITALO
;   TITLE OF INVENTION: GROWTH FACTOR
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;   STREET: 1200 G Street, NW, Suite 700
;   CITY: Washington
;   STATE: DC
;   COUNTRY: United States of America
;   ZIP: 20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/915,795
;   FILING DATE:
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: EVANS, Joseph D.
;   REGISTRATION NUMBER: 26,269
;   REFERENCE/DOCKET NUMBER: 1064/42983
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 628-8800
;   TELEFAX: (202) 628-8844
;   TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 321 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   ORIGINAL SOURCE:
;   TISSUE TYPE: Mouse Lung
US-08-915-795-9

Query Match   77.0%; Score 77; DB 3; Length 321;
Best Local Similarity   87.5%; Pred. No. 0.00042;
Matches 14; Conservative   1; Mismatches 1; Indels 0; Gaps 0;

Qy   2 ASELGKSTNTFCKPPC 17
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Db   121 ASELGKTNTFFKPPC 136

RESULT 7
US-08-915-795-8
; Sequence 8, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
;   APPLICANT: Marc G. ACHEN
;   APPLICANT: Andrew F. WILKS
;   APPLICANT: Steven A. STACKER
;   APPLICANT: Kari ALITALO
;   TITLE OF INVENTION: GROWTH FACTOR
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;   STREET: 1200 G Street, NW, Suite 700
;   CITY: Washington
;   STATE: DC
;   COUNTRY: United States of America
;   ZIP: 20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/915,795
;   FILING DATE:
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: EVANS, Joseph D.
;   REGISTRATION NUMBER: 26,269
;   REFERENCE/DOCKET NUMBER: 1064/42983
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 628-8800
;   TELEFAX: (202) 628-8844
;   TELEX: N/A
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 358 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   ORIGINAL SOURCE:
;   TISSUE TYPE: Mouse Lung
US-08-915-795-8

Query Match   77.0%; Score 77; DB 3; Length 358;
Best Local Similarity   87.5%; Pred. No. 0.00047;
Matches 14; Conservative   1; Mismatches 1; Indels 0; Gaps 0;

Qy   2 ASELGKSTNTFCKPPC 17
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Db   126 ASELGKTTNTFFKPPC 141

RESULT 8
US-08-795-430-11
; Sequence 11, Application US/08795430
; Patent No. 6130071
; GENERAL INFORMATION:
;   APPLICANT: Alitalo, Kari
;   APPLICANT: Joukov, Vladimir
;   TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
;   TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
;   NUMBER OF SEQUENCES: 57
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;   STREET: 6300 Sears Tower, 233 South Wacker Drive
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: United States of America
;   ZIP: 60606-6402
;   COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/795,430
;  FILING DATE:
;  CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: PCT/FI96/00427
;  FILING DATE: 01-AUG-1996
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 08/671,573
;  FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 08/601,132
;  FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 08/585,895
;  FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 08/510,133
;  FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 08/340,011
;  FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
;  NAME: Gass, David A.
;  REGISTRATION NUMBER: 38,153
;  REFERENCE/DOCKET NUMBER: 28967/33691
; TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 312/474-6300
;  TELEFAX: 312/474-0448
;  TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 415 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-08-795-430-11

Query Match           59.0%;    Score 59; DB 3; Length 415;
Best Local Similarity 71.4%;    Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

Qy     4 ELGKSTNTFCKPPC 17
           | |:|||| ||||
Db   139 EFGAATNTFFKPPC 152


RESULT 9
US-09-355-700-11
; Sequence 11, Application US/09355700
; Patent No. 6361946
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research
;   Helsinki University Licensing
;   Alitalo, Kari(U.S. only)
;   Joukov, Vladimir (U.S. only)
;  TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
;   Protein and Gene, Mutants Thereof, and Uses Thereof
;  NUMBER OF SEQUENCES: 59
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;   STREET: 6300 Sears Tower, 233 South Wacker Drive
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: United States of America
;   ZIP: 60606-6402
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/09/355,700
;  FILING DATE: 05-No. 6361946-1999
;  CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 08/795,430
;  FILING DATE: 05-FEB-1997
;  APPLICATION NUMBER: PCT/FI96/00427
;  FILING DATE: 01-AUG-1996
;  APPLICATION NUMBER: 08/671,573
;  FILING DATE: 28-JUN-1996
;  APPLICATION NUMBER: 08/601,132
;  FILING DATE: 14-FEB-1996
;  APPLICATION NUMBER: 08/585,895
;  FILING DATE: 12-JAN-1996
;  APPLICATION NUMBER: 08/510,133
;  FILING DATE: 01-AUG-1995
;  APPLICATION NUMBER: 08/340,011
;  FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
;  NAME: Gass, David A.
;  REGISTRATION NUMBER: 38,153
;  REFERENCE/DOCKET NUMBER: 28967/34140
; TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 312/474-6300
;  TELEFAX: 312/474-0448
;  TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 415 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
;  SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-355-700-11

Query Match           59.0%;    Score 59; DB 4; Length 415;
Best Local Similarity 71.4%;    Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

Qy     4 ELGKSTNTFCKPPC 17
           | |:|||| ||||
Db   139 EFGAATNTFFKPPC 152


RESULT 10
US-08-601-132-41
; Sequence 41, Application US/08601132
; Patent No. 6403088
; GENERAL INFORMATION:
;  APPLICANT: Alitalo, Kari
;  APPLICANT: Joukov, Vladimir
;  TITLE OF INVENTION: Receptor Ligand
;  NUMBER OF SEQUENCES: 41
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;   STREET: 6300 Sears Tower, 233 South Wacker Drive
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: United States of America
;   ZIP: 60606-6402
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/601,132
;  FILING DATE:
;  CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
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Query Match   59.0%;   Score 59; DB 4; Length 415;
Best Local Similarity 71.4%; Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy     4  ELGKSTNTFCKPPC  17
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Db   139  EFGAATNTFFKPPC 152
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RESULT 12
US-08-795-430-13
; Sequence 13, Application US/08795430
; Patent No. 6130071
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,430
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33691
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 418 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-430-13

Query Match   59.0%;   Score 59; DB 3; Length 418;
Best Local Similarity 71.4%; Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/33118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-601-132-41

Query Match   59.0%;   Score 59; DB 4; Length 415;
Best Local Similarity 71.4%; Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy     4  ELGKSTNTFCKPPC  17
          | | :|||| ||||
Db   139  EFGAATNTFFKPPC 152
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RESULT 11
US-08-671-573B-41
; Sequence 41, Application US/08671573B
; Patent No. 6645933
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Receptor Ligand
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671,573B
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-671-573B-41

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Qy       4 ELGKSTNTFCKPPC 17
           | |.:||||||||||
Db     142 EFGATTNTFFKPPC 155


RESULT 13
US-09-355-700-13
; Sequence 13, Application US/09355700
; Patent No. 6361946
; GENERAL INFORMATION:
;   APPLICANT: Ludwig Institute for Cancer Research
;             Helsinki University Licensing
;             Alitalo, Kari(U.S. only)
;             Joukov, Vladimir (U.S. only)
;   TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
;             Protein and Gene, Mutants Thereof, and Uses Thereof
;   NUMBER OF SEQUENCES: 59
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;     STREET: 6300 Sears Tower, 233 South Wacker Drive
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: United States of America
;     ZIP: 60606-6402
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/355,700
;     FILING DATE: 05-No. 6361946-1999
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/795,430
;     FILING DATE: 05-FEB-1997
;     APPLICATION NUMBER: PCT/FI96/00427
;     FILING DATE: 01-AUG-1996
;     APPLICATION NUMBER: 08/671,573
;     FILING DATE: 28-JUN-1996
;     APPLICATION NUMBER: 08/601,132
;     FILING DATE: 14-FEB-1996
;     APPLICATION NUMBER: 08/585,895
;     FILING DATE: 12-JAN-1996
;     APPLICATION NUMBER: 08/510,133
;     FILING DATE: 01-AUG-1995
;     APPLICATION NUMBER: 08/340,011
;     FILING DATE: 14-NOV-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Gass, David A.
;     REGISTRATION NUMBER: 38,153
;     REFERENCE/DOCKET NUMBER: 28967/34140
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312/474-6300
;     TELEFAX: 312/474-0448
;     TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 13:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 418 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-355-700-13

Query Match             59.0%;  Score 59;  DB 4;  Length 418;
Best Local Similarity   71.4%;  Pred. No. 0.29;
Matches   10;  Conservative   1;  Mismatches   3;  Indels   0;  Gaps   0;

Qy       4 ELGKSTNTFCKPPC 17
           | |.:||||||||||
Db     142 EFGATTNTFFKPPC 155
```

```
RESULT 14
US-09-355-700-59
; Sequence 59, Application US/09355700
; Patent No. 6361946
; GENERAL INFORMATION:
;   APPLICANT: Ludwig Institute for Cancer Research
;             Helsinki University Licensing
;             Alitalo, Kari(U.S. only)
;             Joukov, Vladimir (U.S. only)
;   TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
;             Protein and Gene, Mutants Thereof, and Uses Thereof
;   NUMBER OF SEQUENCES: 59
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;     STREET: 6300 Sears Tower, 233 South Wacker Drive
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: United States of America
;     ZIP: 60606-6402
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/355,700
;     FILING DATE: 05-No. 6361946-1999
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/795,430
;     FILING DATE: 05-FEB-1997
;     APPLICATION NUMBER: PCT/FI96/00427
;     FILING DATE: 01-AUG-1996
;     APPLICATION NUMBER: 08/671,573
;     FILING DATE: 28-JUN-1996
;     APPLICATION NUMBER: 08/601,132
;     FILING DATE: 14-FEB-1996
;     APPLICATION NUMBER: 08/585,895
;     FILING DATE: 12-JAN-1996
;     APPLICATION NUMBER: 08/510,133
;     FILING DATE: 01-AUG-1995
;     APPLICATION NUMBER: 08/340,011
;     FILING DATE: 14-NOV-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Gass, David A.
;     REGISTRATION NUMBER: 38,153
;     REFERENCE/DOCKET NUMBER: 28967/34140
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312/474-6300
;     TELEFAX: 312/474-0448
;     TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 59:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 160 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: not relevant
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-355-700-59

Query Match             58.0%;  Score 58;  DB 4;  Length 160;
Best Local Similarity   71.4%;  Pred. No. 0.16%;
Matches   10;  Conservative   1;  Mismatches   3;  Indels   0;  Gaps   0;

Qy       4 ELGKSTNTFCKPPC 17
           | |.:||||| ||||
Db      72 EFGVATNTFFKPPC 85


RESULT 15
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US-09-431-888-7
; Sequence 7, Application US/09431888A
; Patent No. 6541008
; GENERAL INFORMATION:
; APPLICANT: Wise, Lyn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stacker, Stephen
; TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
; TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
; TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence Listing for 09/431,833
; Patent No. 6541008
; CURRENT APPLICATION NUMBER: US/09/431,888A
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/106,689
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/106,800
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-888-7

Query Match   58.0%;   Score 58; DB 4; Length 228;
Best Local Similarity   71.4%;   Pred. No. 0.23;
Matches   10; Conservative   1; Mismatches   3; Indels   0; Gaps   0;

Qy   4 ELGKSTNTFCKPPC 17
            | | :||| ||||
Db   52 EFGVATNTFFKPPC 65

Search completed: September 5, 2004, 10:21:58
Job time : 16.1111 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:47:29 ; Search time 6.90909 Seconds
           (without alignments)
           125.302 Million cell updates/sec

Title: US-09-761-636A-9
Perfect score: 55
Sequence: 1 CCNEESLIC 9
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : PIR 78:*
            1: piri:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	81.8	120	2	A33787	vascular endotheli
2	45	81.8	133	2	B49530	vascular endotheli
3	45	81.8	146	2	S57956	ovine vascular end
4	45	81.8	190	2	B40080	vascular endotheli
5	42	76.4	190	2	B44881	vascular endotheli
6	42	76.4	190	2	A35987	glioma-derived vas
7	42	76.4	214	2	A44881	vascular endotheli
8	41	74.5	190	2	S52130	vascular endotheli
9	41	74.5	232	2	A41551	vascular endotheli
10	40	72.7	82	2	E36787	hypothetical prote
11	39	70.9	162	2	T01973	hypothetical prote
12	39	70.9	419	2	S69207	vascular endotheli
13	37	67.3	92	1	NFHO2	neurophysin 2 - ho
14	37	67.3	107	1	NVWH2F	vasopressin / neur
15	37	67.3	144	2	A29101	vasopressin / neur
16	37	67.3	147	1	NVSH2	vasopressin / neur
17	37	67.3	164	1	NVHU2	vasopressin / neur
18	37	67.3	166	1	NVBO2	vasopressin / neur
19	37	67.3	166	1	NVPG2	vasopressin / neur
20	36	65.5	73	2	F85358	hypothetical prote
21	36	65.5	74	2	G85358	stress responsive
22	36	65.5	101	2	S07514	gene 5.3 protein -
23	36	65.5	149	2	A41236	placental growth f
24	36	65.5	261	2	D90123	hypothetical prote
25	36	65.5	328	2	AB0021	LacI-family transc
26	36	65.5	818	2	F96586	hypothetical prote
27	36	65.5	1115	2	A45761	Ca2+-transporting
28	36	65.5	3655	2	T38084	TRAP-like protein
29	35	63.6	128	2	I51295	vascular endotheli
30	35	63.6	148	2	D49530	16K vascular endot
31	35	63.6	158	2	A56125	placental growth f
32	35	63.6	228	2	T39386	probable G1-S-spec
33	35	63.6	354	2	S59521	mucin 5ac - mouse
34	35	63.6	416	2	G86232	cysteine proteinas
35	35	63.6	477	2	S53362	mucin 5AC (clone J
36	35	63.6	1058	2	JC1254	ubiquitin-protein
37	35	63.6	1058	2	A38564	ubiquitin-protein
38	35	63.6	4427	2	PN0637	polyketide synthas
39	34.5	62.7	351	2	T42421	hypothetical prote
40	34.5	62.7	1778	2	T50074	probable nucleopor
41	34	61.8	129	2	AD0255	probable phage ant
42	34	61.8	166	2	JN0248	platelet-derived g
43	34	61.8	196	2	A37359	platelet-derived g
44	34	61.8	196	2	B28964	platelet-derived g
45	34	61.8	196	2	A48851	platelet-derived g

ALIGNMENTS

RESULT 1
A33787
vascular endothelial growth factor (version 1) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 05-Nov-1999
C;Accession: A33787
R;Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisp
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
A;Title: Vascular endothelial growth factor: a new member of the platelet-derived growth
A;Reference number: A33787; MUID:90121225; PMID:2610687
A;Accession: A33787
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <TIS>
A;Cross-references: GB:M33750; NID:g163810; PIDN:AAA30805.1; PID:g163811
C;Keywords: alternative splicing

Query Match   81.8%; Score 45; DB 2; Length 120;
Best Local Similarity   77.8%; Pred. No. 1.4;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
         |||:|||||
Db 59 CCNDESLEC 67

RESULT 2
B49530
vascular endothelial growth factor homolog A2R, 14.7K - Orf virus
C;Species: Orf virus
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: B49530
R;Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
J. Virol. 68, 84-92, 1994
A;Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus orf
A;Reference number: A49530; MUID:94076465; PMID:8254780
A;Contents: NZ2
A;Accession: B49530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <LYT>
A;Cross-references: GB:S67520; NID:g456897; PIDN:AAB29220.1; PID:g456899
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:141420, NCBIP:141425)

Query Match   81.8%; Score 45; DB 2; Length 133;
Best Local Similarity   77.8%; Pred. No. 1.5;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
         |||:|||||
Db 70 CCNDESLEC 78

RESULT 3
S57956
ovine vascular endothelial growth factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C;Accession: S57956
R;Redmer, D.A.; Dai, Y.; Li, J.; Jones, S.C.; Moor, R.M.
submitted to the EMBL Data Library, July 1995
A;Reference number: S57956
A;Accession: S57956
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <RED>
A;Cross-references: EMBL:X89506; NID:g899350; PIDN:CAA61677.1; PID:g899351

Query Match   81.8%; Score 45; DB 2; Length 146;
Best Local Similarity   77.8%; Pred. No. 1.7;
      Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
           |||:|||||
Db   85 CCNDESLEC 93

RESULT 4
B40080
vascular endothelial growth factor precursor (version 2) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Nov-1999
C;Accession: B40080; B33787; A33255
R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1306-1309, 1989
A;Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
A;Reference number: A40080; MUID:90069608; PMID:2479986
A;Accession: B40080
A;Molecule type: mRNA
A;Residues: 1-190 <LEU>
A;Cross-references: GB:M32976; NID:g163006; PIDN:AAA30502.1; PID:g163007
R;Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisp
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
A;Title: Vascular endothelial growth factor: a new member of the platelet-derived growth
A;Reference number: A33787; MUID:90121225; PMID:2610687
A;Accession: B33787
A;Molecule type: mRNA
A;Residues: 27-190 <TIS>
A;Cross-references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809
R;Ferrara, N.; Henzel, W.J.
Biochem. Biophys. Res. Commun. 161, 851-858, 1989
A;Title: Pituitary follicular cells secrete a novel heparin-binding growth factor specif
A;Reference number: A33255; MUID:89286596; PMID:2735925
A;Accession: A33255
A;Molecule type: protein
A;Residues: 27-31 <FER>
C;Keywords: alternative splicing; glycoprotein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-190/Product: vascular endothelial growth factor #status predicted <MAT>
F;100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   81.8%; Score 45; DB 2; Length 190;
Best Local Similarity   77.8%; Pred. No. 2;
      Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
           |||:|||||
Db   85 CCNDESLEC 93

RESULT 5
B44881
vascular endothelial growth factor-1 precursor - mouse
C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Nov-1999
C;Accession: B44881; A43351; A61029
R;Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A;Title: Expression of vascular endothelial growth factor during embryonic angiogenesis
A;Reference number: A44881; MUID:92274860; PMID:1592003
A;Accession: B44881
A;Molecule type: mRNA
A;Residues: 1-190 <BRE>
A;Cross-references: GB:S38083; NID:g249858; PIDN:AAB22253.1; PID:g249859
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBIP:107623)
R;Claffey, K.P.; Wilkison, W.O.; Spiegelman, B.M.
J. Biol. Chem. 267, 16317-16322, 1992
A;Title: Vascular endothelial growth factor. Regulation by cell differentiation and act
A;Reference number: A43351; MUID:92355593; PMID:1644816
A;Accession: A43351
A;Molecule type: mRNA
A;Residues: 1-116, ER ,119-190 <CLA>
A;Cross-references: GB:M95200; NID:g202350; PIDN:AAA40547.1; PID:g202351
A;Note: sequence extracted from NCBI backbone (NCBIN:110665, NCBIP:110675)
R;Rosenthal, R.A.; Megyesi, J.F.; Henzel, W.J.; Ferrara, N.; Folkman, J.
Growth Factors 4, 53-59, 1990
A;Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelial
A;Reference number: A61029; MUID:91197543; PMID:2085441
A;Accession: A61029
A;Molecule type: protein
A;Residues: 27-38 <ROS>
C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein; mi

Query Match   76.4%; Score 42; DB 2; Length 190;
Best Local Similarity   66.7%; Pred. No. 6.3;
      Matches   6; Conservative   2; Mismatches   2; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
           |||:|:|:|
Db   85 CCNDEALEC 93

RESULT 6
A35987
glioma-derived vascular endothelial cell growth factor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Nov-1999
C;Accession: A35987
R;Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Hope
Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990
A;Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is h
A;Reference number: A35987; MUID:90207249; PMID:2320579
A;Accession: A35987
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <CON>
A;Cross-references: GB:M32167; NID:g204287; PIDN:AAA41211.1; PID:g204288

Query Match   76.4%; Score 42; DB 2; Length 190;
Best Local Similarity   66.7%; Pred. No. 6.3;
      Matches   6; Conservative   2; Mismatches   2; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
           |||:|:|:|
Db   85 CCNDEALEC 93

RESULT 7
A44881
vascular endothelial growth factor-3 precursor - mouse
N;Contains: vascular endothelial growth factor-2; vascular permeability factor
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C;Accession: A44881; C44881; A60932; S52136
R;Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992

A;Title: Expression of vascular endothelial growth factor during embryonic angiogenesis
A;Reference number: A44881; MUID:92274860; PMID:1592003
A;Accession: A44881
A;Molecule type: mRNA
A;Residues: 1-214 <BRE>
A;Cross-references: GB:S37052; NID:g249856; PIDN:AAB22252.1; PID:g249857
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:104677, NCBIP:104678)
A;Accession: C44881
A;Molecule type: mRNA
A;Residues: 1-140,209-214 <BR2>
A;Cross-references: GB:S38100; NID:g249860; PIDN:AAB22254.1; PID:g249861
A;Note: sequence extracted from NCBI backbone (NCBIN:107624, NCBIP:107625)
R;Clauss, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; Pan, Y.C.
J. Exp. Med. 172, 1535-1545, 1990
A;Title: Vascular permeability factor: a tumor-derived polypeptide that induces endothel
A;Reference number: A60932; MUID:91079755; PMID:2258694
A;Accession: A60932
A;Molecule type: protein
A;Residues: 27-33 <CLA>
R;Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
Biochim. Biophys. Acta 1224, 365-370, 1994
A;Title: Enhanced expression of multiple forms of VEGF is associated with spontaneous im
A;Reference number: S52136; MUID:95101726; PMID:7803491
A;Accession: S52136
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-46 <SUG>
C;Comment: Homodimers could be demonstrated for recombinant VEGF-2 but not VEGF-3.
C;Keyword: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homodimer;
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-214/Product: vascular endothelial growth factor-3 #status experimental <MAT>

Query Match   76.4%;   Score 42;   DB 2;   Length 214;
Best Local Similarity   66.7%;   Pred. No. 6.9;
Matches   6; Conservative   2; Mismatches   2; Indels   0; Gaps   0;

```
Qy    1 CCNEESLIC 9
          | |.|:|:||
Db   85 CCNDEALEC 93
```

RESULT 8
S52130
vascular endothelial growth factor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: S52130
R;Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.
Biochim. Biophys. Acta 1260, 235-238, 1995
A;Title: Nucleotide sequence and expression of the porcine vascular endothelial growth f
A;Reference number: S52130; MUID:95143284; PMID:7841203
A;Accession: S52130
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <SHA>
A;Cross-references: GB:X81380; NID:g587559; PIDN:CAA57143.1; PID:g587560

Query Match   74.5%;   Score 41;   DB 2;   Length 190;
Best Local Similarity   66.7%;   Pred. No. 9.2;
Matches   6; Conservative   1; Mismatches   1; Indels   2; Gaps   0;

```
Qy    1 CCNEESLIC 9
          | |.|:|:||
Db   85 CCNDEGLEC 93
```

RESULT 9
A41551
vascular endothelial growth factor 206 precursor - human
N;Alternate names: vascular permeability factor
N;Contains: vascular endothelial growth factor 121 (VEGF 121); VEGF 165; VEGF 189; VEGF
C;Species: Homo sapiens (man)

C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
C;Accession: A41551; C41551; B41551; A40454; C40454; A40079; A40080; JQ1463; JQ
R;Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W.
Mol. Endocrinol. 5, 1806-1814, 1991
A;Title: The vascular endothelial growth factor family: identification of a fourth mole
A;Reference number: A41551; MUID:92168017; PMID:1791831
A;Accession: A41551
A;Molecule type: mRNA
A;Residues: 1-232 <HOU1>
A;Cross-references: GB:S85192; NID:g246155; PID:g246156
A;Accession: C41551
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-140,'N',183-232 <HOU2>
A;Accession: B41551
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-141,227-232 <HOU>
R;Tischer, E.; Mitchell, R.; Hartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.; Al
J. Biol. Chem. 266, 11947-11954, 1991
A;Title: The human gene for vascular endothelial growth factor. Multiple protein forms a
A;Reference number: A40454; MUID:91268072; PMID:1711045
A;Accession: A40454
A;Molecule type: DNA
A;Residues: 1-165,183-232 <TI1>
A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976; GB
A;Accession: B40454
A;Molecule type: DNA
A;Residues: 1-140,'N',183-232 <TI2>
A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63977; GB
A;Accession: C40454
A;Molecule type: DNA
A;Residues: 1-141,227-232 <TI3>
A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63978
R;Keck, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D.T.
Science 246, 1309-1312, 1989
A;Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.
A;Reference number: A40079; MUID:90069609; PMID:2479987
A;Accession: A40079
A;Molecule type: mRNA
A;Residues: 1-165,183-232 <KEC>
A;Cross-references: GB:M27281; NID:g340300; PIDN:AAA36807.1; PID:g340301
R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1306-1309, 1989
A;Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
A;Reference number: A40080; MUID:90069608; PMID:2479986
A;Accession: A40080
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-140,'N',183-232 <LEU>
A;Cross-references: GB:M32977; NID:g181970; PIDN:AAA35789.1; PID:g181971
R;Weindel, K.; Marme, D.; Weich, H.A.
Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992
A;Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial
A;Reference number: JQ1463; MUID:92231879; PMID:1567395
A;Accession: JQ1463
A;Residues: 1-140,'N',183-232 <WEI>
A;Cross-references: EMBL:X62568; NID:g37658; PIDN:CAA44447.1; PID:g37659
A;Experimental source: AIDS-Kaposi's sarcoma cell
A;Accession: JQ1464
A;Molecule type: mRNA
A;Residues: 1-140,'N',227-232 <WE2>
A;Experimental source: AIDS-Kaposi's sarcoma cell
R;Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Monsell, R.; Siegel, N.; Hay
J. Biol. Chem. 264, 20017-20024, 1989
A;Title: Human vascular permeability factor. Isolation from U937 cells.
A;Reference number: A34492; MUID:90062112; PMID:2584205
A;Accession: A34492
A;Molecule type: protein
A;Residues: 27-36;43-49,'R',72-76,'Q',78-81;59-71 <CON>
C;Comment: The most common of several alternatively spliced forms is VEGF 165.

C;Genetics:
A;Gene: GDB:VEGF
A;Cross-references: GDB:132244; OMIM:192240
A;Map position: 6p21-6p12
C;Function:
A;Description: promotes fluid and protein leakage from blood vessels
C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; extracellular pro
F;1-232/Product: vascular endothelial growth factor 206 precursor #status predicted <V20
F;1-165,183-232/Product: vascular endothelial growth factor 189 precursor #status predic
F;1-141,227-232/Product: vascular endothelial growth factor 121 precursor #status predic
F;1-26/Domain: signal sequence #status predicted <SIG>
F;101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   74.5%; Score 41; DB 2; Length 232;
Best Local Similarity 66.7%; Pred. No. 11;
Matches   6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy   1 CCNEESLIC 9
         ||| |||||
Db   86 CCNDEGLEC 94

RESULT 10
E36787
hypothetical protein ORF13 - ictalurid herpesvirus 1 (strain auburn 1)
C;Species: ictalurid herpesvirus 1
A;Note: host Ictalurus punctatus (channel catfish)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C;Accession: E36787
R;Davison, A.J.
submitted to GenBank, January 1992
A;Description: Channel catfish virus: a new type of herpesvirus.
A;Reference number: A36804
A;Accession: E36787
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M75136; NID:g331209; PIDN:AAA88116.1; PID:g331223
R;Davison, A.J.
Virology 186, 9-14, 1992
A;Title: Channel catfish virus: a new type of herpesvirus.
A;Reference number: A39447; MUID:92087490; PMID:1727613
A;Contents: annotation
A;Note: neither protein nor nucleic acid sequence is given
C;Genetics:
A;Gene: 13
C;Keywords: DNA binding; zinc finger

Query Match   72.7%; Score 40; DB 2; Length 82;
Best Local Similarity 66.7%; Pred. No. 7.2;
Matches   6; Conservative 1; Mismatches 1; Indels 2; Gaps 0;

Qy   1 CCNEESLIC 9
         ||| ||||
Db   11 CCNPMSLLC 19

RESULT 11
T01973
hypothetical protein T9A4.2 - Arabidopsis thaliana
N;Alternate names: hypothetical protein F24G24.40
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 14-May-1999
C;Accession: T01973; T04039
R;Zidanic, M.; McQuerry, Y.; Smith, A.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of A. thaliana T9A4.
A;Reference number: Z14478
A;Accession: T01973
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-162 <ZID>
A;Cross-references: EMBL:AF096373; NID:g3695400; PID:g3695405
A;Experimental source: cultivar Columbia
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15184
A;Accession: T04039
A;Molecule type: DNA
A;Residues: 1-162 <BEV>
A;Cross-references: EMBL:AL049488
A;Experimental source: cultivar Columbia; BAC clone F24G24
C;Genetics:
A;Map position: 4
A;Introns: 67/3
A;Note: T9A4.2; F24G24.40

Query Match   70.9%; Score 39; DB 2; Length 162;
Best Local Similarity 44.4%; Pred. No. 18;
Matches   4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCNEESLIC 9
         || |:::::|
Db   17 CCSDEAVLC 25

RESULT 12
S69207
vascular endothelial growth factor C precursor - human
N;Alternate names: FLT4 ligand DHM
C;Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999
C;Accession: S69207; S61795; S71443; S69208; G02659
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela,
EMBO J. 15, 1751, 1996
A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand f
A;Reference number: S69207; MUID:96203094; PMID:8612600
A;Accession: S69207
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-419 <JOU>
A;Cross-references: EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PID:g11820
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela,
EMBO J. 15, 290-298, 1996
A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (
A;Reference number: S61795; MUID:96178224; PMID:8617204
A;Accession: S61795
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 70-419 <JOU1>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
A;Molecule type: protein
A;Residues: 'X',104-120 <JOU2>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and s
A;Reference number: S69208
A;Accession: S69208
A;Molecule type: mRNA
A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAB85214.1; PID:g1150989
R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
A;Accession: G02659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-419 <MOR>
A;Cross-references: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427
C;Genetics:
A;Gene: GDB:VEGFC; VRP
A;Cross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>

F;13-102/Domain: propeptide #status predicted <PRO>
F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>
Query Match   70.9%;   Score 39; DB 2; Length 419;
Best Local Similarity   66.7%;   Pred. No. 36;
Matches   6; Conservative   0; Mismatches   0; Indels   3; Gaps   0;

Qy   1 CCNEESLIC 9
            ||||||| :
Db   165 CCNSEGLQC 173

RESULT 13
NFHO2
neurophysin 2 - horse (tentative sequence) (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 22-May-1981 #sequence_revision 22-May-1981 #text_change 31-Mar-2000
C;Accession: A01444
R;Chauvet, M.T.; Codogno, P.; Chauvet, J.; Acher, R.
FEBS Lett. 80, 374-376, 1977
A;Title: Phylogeny of the neurophysins: complete amino acid sequence of horse MSEL-neuro
A;Reference number: A01444; MUID:77246829; PMID:891988
A;Accession: A01444
A;Molecule type: protein
A;Residues: 1-92 <CHA>
C;Superfamily: oxytocin-neurophysin
C;Keywords: hormone; hypothalamus
F;7-51,10-24,18-41,25-31,58-70,64-82,71-76/Disulfide bonds: #status predicted

Query Match   67.3%;   Score 37; DB 1; Length 92;
Best Local Similarity   62.5%;   Pred. No. 24;
Matches   5; Conservative   2; Mismatches   2; Indels   1; Gaps   0;

Qy   1 CCNEESLI 8
            ||||:||| :
Db   70 CCNDESCV 77

RESULT 14
NVWH2F
vasopressin / neurophysin 2 precursor - finback whale (tentative sequence) (fragment)
N;Contains: Arg-vasopressin; neurophysin 2
C;Species: Balaenoptera physalus (finback whale, common rorqual)
C;Date: 18-Aug-1982 #sequence_revision 05-Jan-1996 #text_change 31-Mar-2000
C;Accession: B93147; A91447; A01446
R;Acher, R.; Chauvet, J.; Chauvet, M.T.
Nature 201, 191-192, 1964
A;Title: Isolation of finback whale oxytocin and vasopressin.
A;Reference number: A93147
A;Accession: B93147
A;Molecule type: protein
A;Residues: 1-9 <ACH>
R;Chauvet, M.T.; Codogno, P.; Chauvet, J.; Acher, R.
FEBS Lett. 88, 91-93, 1978
A;Title: Phylogeny of neurophysins. Complete amino acid sequence of whale (Balaenoptera
A;Reference number: A91447; MUID:78148313; PMID:639997
A;Accession: A91447
A;Molecule type: protein
A;Residues: 13-107 <CHA>
C;Superfamily: oxytocin-neurophysin
C;Keywords: amidated carboxyl end; glycoprotein; hormone; hypothalamus
F;1-9/Product: Arg-vasopressin #status experimental <VAS>
F;13-107/Product: neurophysin 2 #status experimental <NF2>
F;1-6/Disulfide bonds: #status experimental
F;9/Modified site: amidated carboxyl end (Gly) (amide in mature form from following glyc
F;22-66,25-39,33-56,40-46,73-85,79-97,86-91/Disulfide bonds: #status predicted
A;Note: some residues may have been positioned only by homology with other neurophysins
C;Comment: Glycine is placed at 10 and X's at 11 and 12 by homology with the complete se
C;Function:
A;Description: vasopressin is a hypothalmic peptide hormone that is an antidiuretic and,
ein for vasopressin

Query Match   67.3%;   Score 37; DB 1; Length 107;

Best Local Similarity   62.5%;   Pred. No. 27;
Matches   5; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CCNEESLI 8
            ||||:||| :
Db   85 CCNDESCV 92

RESULT 15
A29101
vasopressin / neurophysin 2 precursor - guinea pig
N;Alternate names: copeptin
N;Contains: Arg-vasopressin; neurophysin 2; pituitary glycopeptide
C;Species: Cavia porcellus (guinea pig)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 06-Sep-1996
C;Accession: A29101; S00009; JS0300; A23630
R;Chauvet, M.T.; Rouille, Y.; Chauvet, J.; Acher, R.
FEBS Lett. 210, 40-44, 1987
A;Title: Guinea pig neurohypophysial hormones. Peculiar processing of the three-domain
A;Reference number: A29101; MUID:87105929; PMID:3803579
A;Accession: A29101
A;Molecule type: protein
A;Residues: 1-144 <CHA>
R;Chauvet, J.; Chauvet, M.T.; Acher, R.
FEBS Lett. 217, 180-183, 1987
A;Title: Conformation limited proteolysis in the common neurophysin-copeptin precursor :
A;Reference number: S00009; MUID:87247214; PMID:3595848
A;Accession: S00009
A;Molecule type: protein
A;Residues: 13-144 <CH4>
R;Chauvet, M.T.; Chauvet, J.; Acher, R.
Int. J. Pept. Protein Res. 30, 676-682, 1987
A;Title: Guinea pig MSEL-neurophysin. Sequence comparison of eight mammalian MSEL-neuro
A;Reference number: JS0300; MUID:88138574; PMID:3435704
A;Accession: JS0300
A;Molecule type: protein
A;Residues: 107-144 <CH3>
C;Superfamily: oxytocin-neurophysin
A;Note: 93-Ala was also found
R;Chauvet, M.T.; Chauvet, J.; Acher, R.
FEBS Lett. 197, 169-172, 1986
A;Title: Guinea pig copeptin. The glycopeptide domain of the vasopressin precursor.
A;Reference number: A23630; MUID:86136563; PMID:3081370
A;Accession: A23630
A;Molecule type: protein
A;Residues: 107-144 <CH3>
C;Superfamily: oxytocin-neurophysin
C;Keywords: amidated carboxyl end; glycoprotein; hormone; hypothalamus
F;1-9/Product: Arg-vasopressin #status experimental <RVP>
F;13-105/Product: neurophysin 2 #status experimental <NF2>
F;107-144/Product: pituitary glycopeptide #status experimental <GCP>
F;1-6/Disulfide bonds: #status experimental
F;9/Modified site: amidated carboxyl end (Gly) (amide in mature form from following glyc
F;22-66,25-39,33-56,40-46,73-85,79-97,86-91/Disulfide bonds: #status predicted
F;112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   67.3%;   Score 37; DB 2; Length 144;
Best Local Similarity   62.5%;   Pred. No. 34;
Matches   5; Conservative   2; Mismatches   2; Indels   1; Gaps   0;

Qy   1 CCNEESLI 8
            ||||:||| :
Db   85 CCNDESCV 92

Search completed: September 5, 2004, 10:01:19
Job time : 7.90909 secs

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: September 5, 2004, 09:38:39 ; Search time 4.09091 Seconds
(without alignments)
114.554 Million cell updates/sec

Title: US-09-761-636A-9
Perfect score: 55
Sequence: 1 CCNEESLIC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	ID	Length	DB	Description
1	55	100.0	VEGD_HUMAN	354	1	O43915 homo sapien
2	49	89.1	VEGD_RAT	326	1	O35251 rattus norv
3	45	81.8	VEGH_ORFN2	133	1	P52584 orf virus (
4	45	81.8	VEGA_SHEEP	146	1	P50412 ovis aries
5	45	81.8	VEGA_CAVPO	164	1	P26617 cavia porce
6	45	81.8	VEGA_BOVIN	190	1	P15691 bos taurus
7	45	81.8	VEGD_MOUSE	358	1	P97946 mus musculu
8	42	76.4	VEGA_MOUSE	214	1	Q00731 mus musculu
9	42	76.4	VEGA_RAT	214	1	P16612 rattus norv
10	41	74.5	VEGA_HORSE	190	1	Q9gkr0 equus cabal
11	41	74.5	VEGA_PIG	190	1	P49151 sus scrofa
12	41	74.5	VEGA_CANFA	214	1	Q9myv3 canis famil
13	41	74.5	VEGA_HUMAN	232	1	P15692 homo sapien
14	40	72.7	VG13_HSVI1	82	1	Q00166 ictalurid h
15	39	70.9	VEGC_RAT	126	1	O35757 rattus norv
16	39	70.9	VEGC_MOUSE	415	1	P97953 mus musculu
17	39	70.9	VEGC_HUMAN	419	1	P49767 homo sapien
18	38	69.1	CX3A_CONQU	15	1	P58841 conus querc
19	38	69.1	PLGF_BOVIN	149	1	Q9xs47 bos taurus
20	37	67.3	NEU2_HORSE	92	1	P01182 equus cabal
21	37	67.3	NEU2_BALPH	107	1	P01184 balaenopter
22	37	67.3	NEU2_CAVPO	144	1	P10769 cavia porce
23	37	67.3	NEU2_SHEEP	147	1	P01181 ovis aries
24	37	67.3	NEU2_HUMAN	164	1	P01185 homo sapien
25	37	67.3	NEU2_BOVIN	166	1	P01180 bos taurus
26	37	67.3	NEU2_PIG	166	1	P01183 sus scrofa
27	37	67.3	VEGA_MESAU	190	1	Q99ps1 mesocricetu
28	36	65.5	RC23_ARATH	73	1	Q9M095 arabidopsis
29	36	65.5	RC24_ARATH	74	1	Q9sui0 arabidopsis
30	36	65.5	Y53_BPT3	101	1	P20327 bacteriopha
31	36	65.5	PLGF_HUMAN	221	1	P49763 homo sapien
32	36	65.5	YAMB_SCHPO	3655	1	Q10064 schizosacch
33	35	63.6	TXN4_SELHA	35	1	P83471 selenocosmi
34	35	63.6	VEGH_ORFN7	148	1	P52585 orf virus (
35	35	63.6	PLGF_MOUSE	158	1	P49764 mus musculu
36	35	63.6	PLGF_RAT	158	1	Q63434 rattus norv
37	35	63.6	VEGA_CHICK	216	1	P52582 gallus gall
38	35	63.6	FASC_STRPU	495	1	Q05634 strongyloce
39	35	63.6	SZ6L_HUMAN	1024	1	Q9byh1 homo sapien
40	35	63.6	UBA1_HUMAN	1058	1	P22314 homo sapien
41	35	63.6	UBA1_MOUSE	1058	1	Q02053 mus musculu
42	35	63.6	UBA1_RABIT	1058	1	Q29504 oryctolagus
43	35	63.6	PKSL_BACSU	4427	1	Q05470 bacillus su
44	34.5	62.7	N189_SCHPO	1778	1	Q9utk4 schizosacch
45	34	61.8	TXH4_SELHU	35	1	P83303 selenocosmi

ALIGNMENTS

RESULT 1
VEGD_HUMAN
ID   VEGD_HUMAN   STANDARD;   PRT;   354 AA.
AC   O43915;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF)
GN   FIGF OR VEGFD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=97349118; PubMed=9205122;
RA   Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=98140120; PubMed=9479493;
RA   Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA   Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT   "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT   between the PIGA and the GRPR genes.";
RL   Genomics 47:207-216(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98118549; PubMed=9435229;
RA   Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,
RA   Alitalo K., Stacker S.A.;
RT   "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT   tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RN   [5]
RP   PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
RX   MEDLINE=20011413; PubMed=10542248;
RA   Stacker S.A., Stenvers K.L., Caesar C., Vitali A., Domagala T.,
RA   Nice E.C., Roufail S., Simpson R.J., Moritz R., Karpanen T.,
RA   Alitalo K., Achen M.G.;
RT   "Biosynthesis of vascular endothelial growth factor-D involves
RT   proteolytic processing which generates non-covalent homodimers.";
RL   J. Biol. Chem. 274:32127-32136(1999).
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC       and endothelial cell growth, stimulating their proliferation and
CC       migration and also has effects on the permeability of blood
CC       vessels. May function in the formation of the venous and lymphatic
CC       vascular systems during embryogenesis, and also in the maintenance
CC       of differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in lung, heart, small
CC       intestine and fetal lung, and at lower levels in skeletal muscle,
CC       colon, and pancreas.
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC       linked by disulfide bonds before secretion. The fully processed
CC       VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC       bound by non-covalent interactions.
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
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DR   EMBL; D89630; BAA24264.1; -.
DR   EMBL; Y12863; CAA73370.1; -.
DR   EMBL; Y12864; CAA73371.1; -.
DR   EMBL; Y12865; CAA73371.1; JOINED.
DR   EMBL; Y12866; CAA73371.1; JOINED.
DR   EMBL; Y12867; CAA73371.1; JOINED.
DR   EMBL; Y12868; CAA73371.1; JOINED.
DR   EMBL; Y12869; CAA73371.1; JOINED.
DR   EMBL; Y12870; CAA73371.1; JOINED.
DR   EMBL; AJ000185; CAA03942.1; -.
DR   EMBL; BC027948; AAH27948.1; -.
DR   HSSP; P15692; 1VPP.
DR   Genew; HGNC:3708; FIGF.
DR   MIM; 300091; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005161; F:platelet-derived growth factor receptor bin. .; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   InterPro; IPR004153; CXXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXXCXC; 3.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL        1     21   POTENTIAL.
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                                    OR 99 (IN A MINOR FORM).
FT   PROPEP       22     88
FT   CHAIN        89    205   VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP      206    354
FT   DOMAIN      222    318   4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT                            X(1,3)-C.
FT   REPEAT      222    237   1 (APPROXIMATE).
FT   REPEAT      258    273   2.
FT   REPEAT      277    293   3.
FT   REPEAT      301    318   4.
FT   DISULFID    111    153   BY SIMILARITY.
FT   DISULFID    142    189   BY SIMILARITY.
FT   DISULFID    146    191   BY SIMILARITY.
FT   DISULFID    136    145   INTERCHAIN (BY SIMILARITY).
FT   DISULFID    145    145   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    155    155   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    185    185   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    287    287   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   354 AA;  40444 MW;  2048D769D735173E CRC64;

Query Match             100.0%;  Score 55;  DB 1;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 0.012;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 CCNEESLIC 9
          |||||||||
Db    145 CCNEESLIC 153


RESULT 2
VEGD_RAT
ID   VEGD_RAT     STANDARD;      PRT;    326 AA.
AC   O35251;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF).
GN   FIGF OR VEGFD.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Yamada Y., Hirata Y., Nezu J., Shimane M.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC       and endothelial cell growth, stimulating their proliferation and
CC       migration and also has effects on the permeability of blood
CC       vessels. May function in the formation of the venous and lymphatic
CC       vascular systems during embryogenesis, and also in the maintenance
CC       of differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-3 (Flt4) receptor (By similarity).
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC       linked by disulfide bonds before secretion. The fully processed
CC       VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC       bound by non-covalent interactions (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
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DR   EMBL; AF014827; AAB66557.1; -.
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DR   HSSP; P15692; 1VPP.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 1.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL        1     21       POTENTIAL.
FT   PROPEP       22     93       POTENTIAL.
FT   CHAIN        94    210       VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP      211    326       POTENTIAL.
FT   DOMAIN      227    317       4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT                                X(1,3)-C.
FT   REPEAT      227    242       1 (APPROXIMATE).
FT   REPEAT      263    278       2.
FT   REPEAT      282    298       3.
FT   REPEAT      306    317       4 (INCOMPLETE).
FT   DISULFID    116    158       BY SIMILARITY.
FT   DISULFID    147    194       BY SIMILARITY.
FT   DISULFID    151    196       BY SIMILARITY.
FT   DISULFID    141    141       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    150    150       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    160    160       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    190    190       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    292    292       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE    326 AA;  37112 MW;  1261APA373596C00 CRC64;

Query Match             89.1%;  Score 49;  DB 1;  Length 326;
Best Local Similarity   77.8%;  Pred. No. 0.12;
Matches    7;  Conservative   2;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      1 CCNEESLIC 9
          ||||||:::|
Db    150 CCNERSVMC 158

RESULT 3
VEGH_ORFN2
ID   VEGH_ORFN2     STANDARD;     PRT;    133 AA.
AC   P52584;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor homolog precursor.
GN   A2R.
OS   Orf virus (strain NZ2) (OV NZ-2).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=10259;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94076465; PubMed=8254780;
RA   Lyttle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.;
RT   "Homologs of vascular endothelial growth factor are encoded by the
RT   poxvirus orf virus.";
RL   J. Virol. 68:84-92(1994).
CC   -!- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   -------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; S67520; AAB29220.2; -.
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DR   HSSP; P15692; 1VPP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    133       VASCULAR ENDOTHELIAL GROWTH FACTOR
FT                                HOMOLOG.
FT   DISULFID     36     78       BY SIMILARITY.
FT   DISULFID     67    112       BY SIMILARITY.
FT   DISULFID     71    114       BY SIMILARITY.
FT   DISULFID     61     61       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     70     70       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     85     85       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE    133 AA;  14715 MW;  917C0F688303OC39 CRC64;

Query Match             81.8%;  Score 45;  DB 1;  Length 133;
Best Local Similarity   77.8%;  Pred. No. 0.26;
Matches    7;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy      1 CCNEESLIC 9
          |||:|:||:|
Db     70 CCNDESLEC 78

RESULT 4
VEGA_SHEEP
ID   VEGA_SHEEP     STANDARD;     PRT;    146 AA.
AC   P50412;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE   permeability factor) (VPF).
GN   VEGF OR VEGFA.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=97117958; PubMed=8958842;
RA   Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,
RA   Reynolds L.P., Moor R.M.;
RT   "Characterization and expression of vascular endothelial growth
RT   factor (VEGF) in the ovine corpus luteum.";
RL   J. Reprod. Fertil. 108:157-165(1996).
CC   -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC       endothelial cell growth. It induces endothelial cell
CC       proliferation, promotes cell migration, inhibits apoptosis, and
CC       induces permeabilization of blood vessels. It binds to the
CC       VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC       heparin (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC       with PlGF (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   -------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; X89506; CAA61677.1; -.
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DR   PIR; S57956; S57956.
DR   HSSP; P15692; 1VPP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW   Heparin-binding; Multigene family.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    146       VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT   DISULFID     51     93       BY SIMILARITY.
FT   DISULFID     82    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    100    100       N-LINKED (GLcNAC...) (POTENTIAL).
SQ   SEQUENCE   146 AA;  17247 MW;  4E792CB557P91760 CRC64;

Query Match             81.8%;  Score 45;  DB 1;  Length 146;
Best Local Similarity   77.8%;  Pred. No. 0.29;
Matches    7;  Conservative   1;  Mismatches   1;  Indels   1;  Gaps   0;

Qy       1  CCNEESLIC 9
            |||:|||-|
Db      85  CCNDESLEC 93

RESULT 5
VEGA_CAVPO
ID   VEGA_CAVPO     STANDARD;      PRT;   164 AA.
AC   P26617;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor A (VEGF-A) (Vascular permeability
DE   factor) (VPF).
GN   VEGF OR VEGFA.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bile duct;
RA   Berse B.;
RL   Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Growth factor active in angiogenesis, and endothelial
CC       cell growth. Induces endothelial proliferation and vascular
CC       permeability (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC       with PlGF (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC       to the extracellular matrix unless released by heparin (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   -------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; M84230; AAA37057.1; -.
DR   HSSP; P15692; 1VGH.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
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DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Angiogenesis; Growth factor; Glycoprotein.
FT   DISULFID     25     67       BY SIMILARITY.
FT   DISULFID     56    101       BY SIMILARITY.
FT   DISULFID     60    103       BY SIMILARITY.
FT   DISULFID     50     50       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     59     59       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     74     74       N-LINKED (GLcNAC...) (POTENTIAL).
SQ   SEQUENCE   164 AA;  19330 MW;  9EB86A81A9D5DCA4 CRC64;

Query Match             81.8%;  Score 45;  DB 1;  Length 164;
Best Local Similarity   77.8%;  Pred. No. 0.32;
Matches    7;  Conservative   1;  Mismatches   1;  Indels   1;  Gaps   0;

Qy       1  CCNEESLIC 9
            |||:|||-|
Db      59  CCNDESLEC 67

RESULT 6
VEGA_BOVIN
ID   VEGA_BOVIN     STANDARD;      PRT;   190 AA.
AC   P15691;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE   permeability factor) (VPF).
GN   VEGF OR VEGFA.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
RX   MEDLINE=9069608; PubMed=2479986;
RA   Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
RT   "Vascular endothelial growth factor is a secreted angiogenic
RT   mitogen.";
RL   Science 246:1306-1309(1989).
RN   [2]
RP   SEQUENCE OF 27-190 FROM N.A. (ISOFORMS ALPHA AND BETA).
RX   MEDLINE=9121225; PubMed=2610687;
RA   Tischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J.,
RA   Lau K., Crisp T., Fiddes J.C., Abraham J.A.;
RT   "Vascular endothelial growth factor: a new member of the platelet-
RT   derived growth factor gene family.";
RL   Biochem. Biophys. Res. Commun. 165:1198-1206(1989).
RN   [3]
RP   SEQUENCE OF 27-31.
RX   MEDLINE=89286596; PubMed=2735925;
RA   Ferrara N., Henzel W.J.;
RT   "Pituitary follicular cells secrete a novel heparin-binding growth
RT   factor specific for vascular endothelial cells.";
RL   Biochem. Biophys. Res. Commun. 161:851-858(1989).
CC   -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC       endothelial cell growth. It induces endothelial cell
CC       proliferation, promotes cell migration, inhibits apoptosis, and
CC       induces permeabilization of blood vessels. It binds to the
CC       VEGFR/Flt-1 and VEGFR2/Kdr receptors.and to heparan sulfate and
CC       heparin (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC       with PlGF (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC       to the extracellular matrix unless released by heparin (By
CC       similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
```

CC   Name=Alpha;
CC   IsoId=P15691-1; Sequence=Displayed;
CC   Name=Beta;
CC   IsoId=P15691-2; Sequence=VSP_004613, VSP_004614;
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   ---
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; M32976; AAA30502.1; -.
DR   EMBL; M31836; AAA30804.1; -.
DR   EMBL; M33750; AAA30805.1; -.
DR   PIR; A33787; A33787.
DR   PIR; B40080; B40080.
DR   HSSP; P15692; 1VGH.
DR   InterPro; IPR002400; GF_Cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS00278; PDGF_2; 1.
KW   Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW   Heparin-binding; Alternative splicing; Multigene family.
FT   SIGNAL   1   26
FT   CHAIN   27   190   VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT   DISULFID   51   93   BY SIMILARITY.
FT   DISULFID   82   127   BY SIMILARITY.
FT   DISULFID   86   129   BY SIMILARITY.
FT   DISULFID   76   76   INTERCHAIN (BY SIMILARITY).
FT   DISULFID   85   85   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   100   100   N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC   139   183   Missing (in isoform Beta).
FT   /FTId=VSP_004613.
FT   VARSPLIC   184   184   R -> K (in isoform Beta).
FT   /FTId=VSP_004614.
SQ   SEQUENCE   190 AA; 22310 MW; EDBF903E46E24789 CRC64;

Query Match   81.8%; Score 45; DB 1; Length 190;
Best Local Similarity   77.8%; Pred. No. 0.37;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
           |||||||||
Db   85 CCNDESLEC 93

RESULT 7
VEGD_MOUSE
ID   VEGD_MOUSE   STANDARD;   PRT;   358 AA.
AC   P97946;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE   growth factor) (FIGF).
GN   FIGF OR VEGFD.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Fibroblast;
RX   MEDLINE=97030254; PubMed=8876195;
RA   Orlandini M., Marconcini L., Ferruzzi R., Oliviero S.;
RT   "Identification of a c-fos-induced gene that is related to the

platelet-derived growth factor/vascular endothelial growth factor
RT   family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=lung;
RX   MEDLINE=97349118; PubMed=9205122;
RA   Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
RN   [3]
RP   DEVELOPMENTAL STAGE.
RX   MEDLINE=98288130; PubMed=9622638;
RA   Avantaggiato V., Orlandini M., Acampora D., Oliviero S., Simeone A.;
RT   "Embryonic expression pattern of the murine figf gene, a growth factor
RT   belonging to platelet-derived growth factor/vascular endothelial
RT   growth factor family.";
RL   Mech. Dev. 73:221-224(1998).
RN   [4]
RP   RECEPTOR SPECIFICITY.
RX   MEDLINE=21276411; PubMed=11279005;
RA   Baldwin M.E., Catimel B., Nice E.C., Roufail S., Hall N.E.,
RA   Stenvers K.L., Karkkainen M.J., Alitalo K., Stacker S.A., Achen M.G.;
RT   "The specificity of receptor binding by vascular endothelial growth
RT   factor-d is different in mouse and man.";
RL   J. Biol. Chem. 276:19166-19171(2001).
CC   -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC   and endothelial cell growth, stimulating their proliferation and
CC   migration and also has effects on the permeability of blood
CC   vessels. May function in the formation of the venous and lymphatic
CC   vascular systems during embryogenesis, and also in the maintenance
CC   of differentiated lymphatic endothelium in adults. Binds and
CC   activates VEGFR-3 (Flt4) receptor.
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in fetal and adult lung.
CC   -!- DEVELOPMENTAL STAGE: Expressed in a dynamic pattern in several
CC   body structures and organs of the embryo such as limb buds,
CC   acoustic ganglion, teeth, heart, anterior pituitary as well as
CC   lung and kidney mesenchyme, liver, derma, and periosteum of the
CC   vertebral column.
CC   -!- INDUCTION: By the transcription factor c-fos.
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC   variety of processed secreted forms with increased activity toward
CC   VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC   linked by disulfide bonds before secretion. The fully processed
CC   VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC   bound by non-covalent interactions (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   ---
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CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; X99572; CAA67892.1; -.
DR   EMBL; D89628; BAA14002.1; -.
DR   HSSP; P15692; 1VPP.
DR   PMMA-2DPAGE; P97946; -.
DR   MGD; MGI:108037; Figf.
DR   GO; GO:0005576; C:extracellular; IDA.
DR   GO; GO:0008083; F:growth factor activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0008283; P:cell proliferation; IDA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 2.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.

DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW   Cleavage on pair of basic residues; Multigene family.
FT   SIGNAL   1   21   POTENTIAL.
FT   PROPEP   22   93   POTENTIAL.
FT   CHAIN   94   210   VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT   PROPEP   211   358   POTENTIAL.
FT   DOMAIN   227   323   4 X 16 AA REPEATS OF C-X(10)-C-X-C-
FT   X(1,3)-C.
FT   REPEAT   227   242   1 (APPROXIMATE).
FT   REPEAT   263   278   2.
FT   REPEAT   282   298   3.
FT   REPEAT   306   323   4.
FT   DISULFID   116   158   BY SIMILARITY.
FT   DISULFID   147   194   BY SIMILARITY.
FT   DISULFID   151   196   BY SIMILARITY.
FT   DISULFID   141   141   INTERCHAIN (BY SIMILARITY).
FT   DISULFID   150   150   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   160   160   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   190   190   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   292   292   N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   358 AA; 40908 MW; 6636B17FBF07037C CRC64;

Query Match   81.8%;   Score 45; DB 1; Length 358;
Best Local Similarity 66.7%; Pred. No. 0.69;
Matches   6; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
            ||||| ::|
Db   150 CCNEEGVMC 158

RESULT 8
VEGA_MOUSE
ID   VEGA_MOUSE   STANDARD;   PRT;   214 AA.
AC   Q00731;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE   permeability factor) (VPF).
GN   VEGF OR VEGFA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS VEGF-1; VEGF-2 AND VEGF-3).
RX   MEDLINE=92274860; PubMed=1592003;
RA   Breier G., Albrecht U., Sterrer S., Risau W.;
RT   "Expression of vascular endothelial growth factor during embryonic
RT   angiogenesis and endothelial cell differentiation.";
RL   Development 114:521-532(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF-1).
RX   MEDLINE=92355593; PubMed=1644816;
RA   Claffey K.P., Wilkison W.O., Spiegelman B.M.;
RT   "Vascular endothelial growth factor. Regulation by cell
RT   differentiation and activated second messenger pathways.";
RL   J. Biol. Chem. 267:16317-16322(1992).
RN   [3]
RP   SEQUENCE OF 1-3 FROM N.A.
RX   MEDLINE=96216498; PubMed=8632007;
RA   Shima D.T., Kuroki M., Deutsch U., Ng Y., Adamis A.P., D'Amore P.A.;
RT   "The mouse gene for vascular endothelial growth factor. Genomic
RT   structure, definition of the transcriptional unit, and
RT   characterization of transcriptional and post-transcriptional
RT   regulatory sequences.";
RL   J. Biol. Chem. 271:3877-3883(1996).
CC   -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC   endothelial cell growth. It induces endothelial cell

CC   proliferation, promotes cell migration, inhibits apoptosis, and
CC   induces permeabilization of blood vessels. It binds to the
CC   VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC   heparin (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC   with PlGF (By similarity).
CC   -!- SUBCELLULAR LOCATION: VEGF-1 and VEGF-2 are secreted while VEGF-3
CC   remains cell-surface associated unless released by heparin.
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=3;
CC   Name=VEGF-3; Synonyms=VEGF188;
CC   IsoId=Q00731-1; Sequence=Displayed;
CC   Name=VEGF-1; Synonyms=VEGF164;
CC   IsoId=Q00731-2; Sequence=VSP_004626, VSP_004627;
CC   Name=VEGF-2; Synonyms=VEGF120;
CC   IsoId=Q00731-3; Sequence=VSP_004628;
CC   -!- TISSUE SPECIFICITY: In developing embryos, expressed mainly in the
CC   choroid plexus, paraventricular neuroepithelium, placenta and
CC   kidney glomeruli. Also found in bronchial epithelium, adrenal
CC   gland and in seminiferous tubules of testis. High expression of
CC   VEGF continues in kidney glomeruli and choroid plexus in adults.
CC   -!- DOMAIN: VEGF-3 contains a basic insert which acts as a cell
CC   retention signal.
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   ---
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; S37052; AAB22252.1; -.
DR   EMBL; S38083; AAB22253.1; -.
DR   EMBL; S38100; AAB22254.1; -.
DR   EMBL; M95200; AAA40547.1; -.
DR   EMBL; U41383; -; NOT_ANNOTATED_CDS.
DR   PIR; A44881; A44881.
DR   PIR; B44881; B44881.
DR   HSSP; P15692; 2VPF.
DR   MGD; MGI:103178; Vegfa.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW   Heparin-binding; Alternative splicing; Multigene family.
FT   SIGNAL   1   26   BY SIMILARITY.
FT   CHAIN   27   214   VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT   DISULFID   51   93   BY SIMILARITY.
FT   DISULFID   82   127   BY SIMILARITY.
FT   DISULFID   86   129   BY SIMILARITY.
FT   DISULFID   76   76   INTERCHAIN (BY SIMILARITY).
FT   DISULFID   85   85   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   100   100   N-LINKED (GLCNAC. . .) (PROBABLE).
FT   VARSPLIC   140   140   K -> N (in isoform VEGF-1).
FT   /FTId=VSP_004626.
FT   VARSPLIC   141   164   Missing (In isoform VEGF-1).
FT   /FTId=VSP_004627.
FT   VARSPLIC   141   208   Missing (In isoform VEGF-2).
FT   /FTId=VSP_004628.
FT   CONFLICT   117   118   GE -> ER (IN REF. 2).
SQ   SEQUENCE   214 AA; 25283 MW; B5540B51E4BB6517 CRC64;

Query Match   76.4%;   Score 42; DB 1; Length 214;
Best Local Similarity 66.7%; Pred. No. 1.4;
Matches   6; Conservative   6; Mismatches   2; Indels   1; Gaps   0;

Qy   1 CCNEESLIC 9
            |||:|:||

```
Db          85 CCNDEALEC 93

RESULT 9
VEGA_RAT
ID   VEGA_RAT       STANDARD;      PRT;   214 AA.
AC   P16612; Q9JKX7; Q9QXG6; Q9QXG7;
DT   01-AUG-1990 (Rel. 15, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE   permeability factor) (VPF).
GN   VEGF OR VEGFA.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF-A164), AND SEQUENCE OF 27-190.
RX   MEDLINE=90207249; PubMed=2320579;
RA   Conn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A.,
RA   Palisi T.M., Hope D.A., Thomas K.A.;
RT   "Amino acid and cDNA sequences of a vascular endothelial cell mitogen
RT   that is homologous to platelet-derived growth factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2628-2633(1990).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS VEGF-A188; VEGF-A164; VEGF-A144 AND
RP   VEGF-A120).
RX   MEDLINE=21092309; PubMed=11163598;
RA   Ishii H., Oota I., Takuma T., Inomata K.;
RT   "Developmental expression of vascular endothelial growth factor in the
RT   masseter muscle of rats.";
RL   Arch. Oral Biol. 46:77-82(2001).
RN   [3]
RP   SEQUENCE OF 27-40.
RC   TISSUE=Glial tumor;
RX   MEDLINE=9522143; PubMed=7706320;
RA   Disalvo J., Bayne M.L., Conn G., Kwok P.W., Trivedi P.G.,
RA   Soderman D.D., Palisi T.M., Sullivan K.A., Thomas K.A.;
RT   "Purification and characterization of a naturally occurring vascular
RT   endothelial growth factor.placenta growth factor heterodimer.";
RL   J. Biol. Chem. 270:7717-7723(1995).
CC   -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC       endothelial cell growth. It induces endothelial cell
CC       proliferation, promotes cell migration, inhibits apoptosis, and
CC       induces permeabilization of blood vessels. It binds to the
CC       VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC       heparin (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC       with PlGF (By similarity).
CC   -!- SUBCELLULAR LOCATION: VEGF-A120 is acidic and freely secreted.
CC       VEGF-A164 is more basic, has heparin-binding properties and,
CC       although a signicant proportion remains cell-associated, most is
CC       freely secreted. VEGF-A188 is very basic, it is cell-associated
CC       after secretion and is bound avidly by heparin and the
CC       extracellular matrix, although it may be released as a soluble
CC       form by heparin, heparinase or plasmin (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Comment=Additional isoforms seem to exist;
CC       Name=VEGF-A188;
CC         IsoId=P16612-1; Sequence=Displayed;
CC       Name=VEGF-A164;
CC         IsoId=P16612-2; Sequence=VSP_004629, VSP_004630;
CC       Name=VEGF-A144;
CC         IsoId=P16612-3; Sequence=VSP_004632;
CC       Name=VEGF-A120;
CC         IsoId=P16612-4; Sequence=VSP_004631;
CC   -!- TISSUE SPECIFICITY: Expressed in the pituitary, in brain, in
CC       particularly in supraoptic and paraventricular nuclei and the
CC       choroid plexus. Also found abundantly in the corpus luteum of the
CC       ovary and in kidney glomeruli.
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   -------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; M32167; AAA41211.1; -.
DR   EMBL; AF215725; AAF19211.1; -.
DR   EMBL; AF215726; AAF19212.1; -.
DR   EMBL; AF222779; AAF25958.1; -.
DR   HSSP; P15692; 1VPF.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW   Heparin-binding; Alternative splicing; Multigene family.
FT   SIGNAL        1     26
FT   CHAIN        27    214       VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT   DISULFID     51     93       BY SIMILARITY.
FT   DISULFID     82    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    100    100       N-LINKED (GLCNAC...).
FT   VARSPLIC    140    140       K -> N (in isoform VEGF-A164).
FT                                /FTId=VSP_004629.
FT   VARSPLIC    141    164       Missing (in isoform VEGF-A164).
FT                                /FTId=VSP_004630.
FT   VARSPLIC    141    208       Missing (in isoform VEGF-A120).
FT                                /FTId=VSP_004631.
FT   VARSPLIC    165    208       Missing (in isoform VEGF-A144).
FT                                /FTId=VSP_004632.
FT   CONFLICT    101    101       V -> A (IN REF. 2; AAF19212).
SQ   SEQUENCE   214 AA;  25239 MW;  60FBB876F5304946 CRC64;

Query Match             76.4%;  Score 42;  DB 1;  Length 214;
Best Local Similarity   66.7%;  Pred. No. 1.4;
Matches    6;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    0;

Qy          1 CCNEESLIC 9
              |||:|:|:|
Db         85 CCNDEALEC 93

RESULT 10
VEGA_HORSE
ID   VEGA_HORSE     STANDARD;      PRT;   190 AA.
AC   Q9GKR0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE   permeability factor) (VPF).
GN   VEGF OR VEGFA.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Miura N., Misumi K., Kawahara K., Nakashima M., Fukumitsu S.,
RA   Kawabata H., Uto N., Oka T., Maruyama I., Sakamoto H.;
RT   "Cloning of cDNA and high-level expression of equine vascular
RT   endothelial growth factor (VEGF).";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Growth factor active in angiogenesis, and endothelial
CC       cell growth. Induces endothelial proliferation and vascular
```

```
CC        permeability (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC        with PlGF (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC        to the extracellular matrix unless released by heparin (By
CC        similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed.  Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; AB053350; BAB20890.1; -.
DR   HSSP; P15692; 1VGH.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS00278; PDGF_2; 1.
KW   Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW   Multigene family.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    190       VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT   DISULFID     51     93       BY SIMILARITY.
FT   DISULFID     82    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    100    100       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   190 AA;  22312 MW;  87E9E16439E5F87 CRC64;

Query Match             74.5%;  Score 41;  DB 1;  Length 190;
Best Local Similarity   66.7%;  Pred. No. 1.9;
Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCNEESLIC 9
              |||:| | |
Db         85 CCNDEGLEC 93

RESULT 11
VEGA_PIG
ID   VEGA_PIG       STANDARD;      PRT;    190 AA.
AC   P49151; Q9GLS2;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE   permeability factor) (VPF).
GN   VEGF OR VEGFA.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=95143284; PubMed=7841203;
RA   Sharma H.S., Tang Z.H., Gho B.C.H., Verdouw P.D.;
RT   "Nucleotide sequence and expression of the porcine vascular
RT   endothelial growth factor.";
RL   Biochim. Biophys. Acta 1260:235-238(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Lee T., Canty J.M.;
RT   "PCR cloning of porcine cardiac vascular endothelial growth factor
RT   gene.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC        endothelial cell growth. It induces endothelial cell
CC        proliferation, promotes cell migration, inhibits apoptosis, and
CC        induces permeabilization of blood vessels. It binds to the
CC        VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC        heparin (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC        with PlGF (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC        to the extracellular matrix unless released by heparin (By
CC        similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; X81380; CAA57143.1; -.
DR   EMBL; AF318502; AAG33064.1; -.
DR   PIR; S52130; S52130.
DR   HSSP; P15692; 1VGH.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS00278; PDGF_2; 1.
KW   Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW   Heparin-binding; Multigene family.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    190       VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT   DISULFID     51     93       BY SIMILARITY.
FT   DISULFID     82    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    100    100       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT    102    102       T -> A (IN REF 2).
SQ   SEQUENCE   190 AA;  22368 MW;  04D40BBD7913047F CRC64;

Query Match             74.5%;  Score 41;  DB 1;  Length 190;
Best Local Similarity   66.7%;  Pred. No. 1.9;
Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCNEESLIC 9
              |||:| | |
Db         85 CCNDEGLEC 93

RESULT 12
VEGA_CANFA
ID   VEGA_CANFA     STANDARD;      PRT;    214 AA.
AC   Q9MYV3; Q9XSF3; Q9XSF4; Q9XSF5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE   permeability factor) (VPF).
GN   VEGF OR VEGFA.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF-188).
```

```
Best Local Similarity 66.7%;  Pred. No. 2.1;
Matches  6;  Conservative  1;  Mismatches  2;  Indels  2;  Gaps  0;

Qy        1 CCNEESLIC 9
            |||:||:||
Db       85 CCNDEGLEC 93

RESULT 13
VEGA_HUMAN
ID   VEGA_HUMAN     STANDARD;      PRT;   232 AA.
AC   P15692; O60720; O75875; Q16889; Q96L82; Q96NW5; Q9H1W8; Q9H1W9;
AC   Q9UH58; Q9UL23;
DT   01-APR-1990 (Rel. 14, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE   permeability factor) (VPF).
GN   VEGF OR VEGFA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS VEGF189 AND VEGF165).
RX   MEDLINE=90069608; PubMed=2479986;
RA   Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
RT   "Vascular endothelial growth factor is a secreted angiogenic
RT   mitogen.";
RL   Science 246:1306-1309(1989).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF189), AND PARTIAL SEQUENCE.
RX   MEDLINE=90069609; PubMed=2479987;
RA   Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J.,
RA   Connolly D.T.;
RT   "Vascular permeability factor, an endothelial cell mitogen related to
RT   PDGF.";
RL   Science 246:1309-1312(1989).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF189).
RX   MEDLINE=91268072; PubMed=1711045;
RA   Tischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D.,
RA   Fiddes J.C., Abraham J.A.;
RT   "The human gene for vascular endothelial growth factor. Multiple
RT   protein forms are encoded through alternative exon splicing.";
RL   J. Biol. Chem. 266:11947-11954(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF206).
RX   MEDLINE=92168017; PubMed=1791181;
RA   Houck K.A., Ferrara N., Winer J., Cachianes G., Li B., Leung D.W.;
RT   "The vascular endothelial growth factor family: identification of a
RT   fourth molecular species and characterization of alternative splicing
RT   of RNA.";
RL   Mol. Endocrinol. 5:1806-1814(1991).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF165).
RX   MEDLINE=92231879; PubMed=1567395;
RA   Weindel K., Marme D., Weich H.A.;
RT   "AIDS-associated Kaposi's sarcoma cells in culture express vascular
RT   endothelial growth factor.";
RL   Biochem. Biophys. Res. Commun. 183:1167-1174(1992).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF145).
RX   MEDLINE=97207275; PubMed=9054410;
RA   Poltorak Z., Cohen T., Sivan R., Kandelis Y., Spira G., Vlodavsky I.,
RA   Keshet E., Neufeld G.;
RT   "VEGF145, a secreted vascular endothelial growth factor isoform that
RT   binds to extracellular matrix.";
RL   J. Biol. Chem. 272:7151-7158(1997).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF183).
RC   TISSUE=Kidney;
RX   MEDLINE=99096474; PubMed=9878851;
RX   MEDLINE=20125516; PubMed=10661874;
RA   Scheidegger P., Weiglhofer W., Suarez S., Kaser-Hotz B., Steiner R.,
RA   Ballmer-Hofer K., Jaussi R.;
RT   "Vascular endothelial growth factor (VEGF) and its receptors in tumor-
RT   bearing dogs.";
RL   Biol. Chem. 380:1449-1454(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS VEGF-188, VEGF-182 AND VEGF-164).
RC   TISSUE=Heart;
RA   Jingjing L., Roque R.S.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC       endothelial cell growth. It induces endothelial cell
CC       proliferation, promotes cell migration, inhibits apoptosis, and
CC       induces permeabilization of blood vessels. It binds to the
CC       VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC       heparin (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC       with PlGF (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC       to the extracellular matrix unless released by heparin (By
CC       similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=VEGF-188;
CC         IsoId=Q9MYV3-1; Sequence=Displayed;
CC       Name=VEGF-182;
CC         IsoId=Q9MYV3-2; Sequence=VSP_004617;
CC       Name=VEGF-164;
CC         IsoId=Q9MYV3-3; Sequence=VSP_004615, VSP_004616;
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AJ133758; CAB82426.1; -.
DR   EMBL; AF133750; AAD29684.1; -.
DR   EMBL; AF133249; AAD29683.1; -.
DR   EMBL; AF133248; AAD29682.1; -.
DR   HSSP; P15692; 1VGH.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW   Heparin-binding; Alternative splicing; Multigene family.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    214       VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT   DISULFID     51     93       BY SIMILARITY.
FT   DISULFID     82    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    100    100       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC    140    140       K -> N (in isoform VEGF-164).
FT                                /FTId=VSP_004615.
FT   VARSPLIC    141    164       Missing (in isoform VEGF-164).
FT                                /FTId=VSP_004616.
FT   VARSPLIC    159    164       Missing (in isoform VEGF-182).
FT                                /FTId=VSP_004617.
FT   CONFLICT    143    143       I -> V (IN REF. 2).
FT   CONFLICT    161    161       P -> S (IN REF. 2).
SQ   SEQUENCE   214 AA;  25175 MW;  0AC980A158C44B27 CRC64;

Query Match      74.5%;  Score 41;  DB 1;  Length 214;
```

RA   Lei J., Jiang A., Pei D.;
RT   "Identification and characterization of a new splicing variant of
RT   vascular endothelial growth factor: VEGF183.";
RL   Biochim. Biophys. Acta 1443:400-406(1998).
RN   [8]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF165).
RC   TISSUE=Breast;
RX   MEDLINE=98119755; PubMed=9450968;
RA   Claffey K.P., Shih S.-C., Mullen A., Dziennis S., Cusick J.L.,
RA   Abrams K.R., Lee S.W., Detmar M.;
RT   "Identification of a human VPF/VEGF 3' untranslated region mediating
RT   hypoxia-induced mRNA stability.";
RL   Mol. Biol. Cell 9:469-481(1998).
RN   [9]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF165).
RC   TISSUE=Hemangioendothelioma;
RA   Murata H., Fukushima J., Hattori S., Okuda K., Yanagi H.;
RT   "Human cDNA for vascular endothelial growth factor isoform
RT   VEGF165.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF148).
RC   TISSUE=Renal glomerulus;
RX   MEDLINE=99394945; PubMed=10464055;
RA   Whittle C.J., Gillespie K.M., Harrison R., Mathieson P.W.,
RA   Harper S.J.;
RT   "Heterogeneous vascular endothelial growth factor (VEGF) isoform mRNA
RT   and receptor mRNA expression in human glomeruli, and the
RT   identification of VEGF148 mRNA, a novel truncated splice variant.";
RL   Clin. Sci. 97:303-312(1999).
RN   [11]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF121).
RA   Sato J.D., Whitney R.G.;
RT   "Human cDNA for vascular endothelial growth factor isoform VEGF121.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [12]
RP   SEQUENCE FROM N.A.
RA   Williams S.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [13]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF165).
RA   Liu J., Peng X., Yuan J., Qiang B.;
RT   "Cloning of vascular endothelial growth factor (VEGF) cDNA.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [14]
RP   SEQUENCE FROM N.A. (ISOFORM VEGF165).
RC   TISSUE=Heart;
RA   Shan Z.X., Yu X.Y., Lin Q.X., Fu Y.H., Zheng M., Tan H.H., Lin S.G.;
RT   "Cloning and identification of vascular endothelial growth factor
RT   isoform VEGF165.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [15]
RP   SEQUENCE OF 23-232 FROM N.A. (ISOFORM VEGF165).
RA   Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA   Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [16]
RP   SEQUENCE OF 114-209 FROM N.A. (ISOFORM VEGF183).
RC   TISSUE=Retina;
RX   MEDLINE=99165303; PubMed=10067980;
RA   Jingjing L., Xue Y., Agarwal N., Roque R.S.;
RT   "Human Muller cells express VEGF183, a novel spliced variant of
RT   vascular endothelial growth factor.";
RL   Invest. Ophthalmol. Vis. Sci. 40:752-759(1999).
RN   [17]
RP   PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.
RX   MEDLINE=90062112; PubMed=2584205;
RA   Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R.,
RA   Siegel N., Haymore B.L., Leimgruber R., Feder J.;
RT   "Human vascular permeability factor. Isolation from U937 cells.";
RL   J. Biol. Chem. 264:20017-20024(1989).
RN   [18]
RP   SEQUENCE OF 27-41.

RX   MEDLINE=93145946; PubMed=7678805;
RA   Fiebich B.L., Jaeger B., Schoellmann C., Weindel K., Wilting J.,
RA   Kochs G., Marme D., Hug H., Weich H.A.;
RT   "Synthesis and assembly of functionally active human vascular
RT   endothelial growth factor homodimers in insect cells.";
RL   Eur. J. Biochem. 211:19-26(1993).
RN   [19]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
RX   MEDLINE=97352774; PubMed=9207067;
RA   Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
RA   de Vos A.M.;
RT   "Vascular endothelial growth factor: crystal structure and functional
RT   mapping of the kinase domain receptor binding site.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
RN   [20]
RP   X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
RX   MEDLINE=98035455; PubMed=9351807;
RA   Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
RT   "The crystal structure of vascular endothelial growth factor (VEGF)
RT   refined to 1.93-A resolution: multiple copy flexibility and receptor
RT   binding.";
RL   Structure 5:1325-1338(1997).
RN   [21]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
RX   MEDLINE=99119204; PubMed=9922142;
RA   Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,
RA   Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;
RT   "Crystal structure of the complex between VEGF and a receptor-blocking
RT   peptide.";
RL   Biochemistry 37:17765-17772(1998).
RN   [22]
RP   STRUCTURE BY NMR OF 34-135.
RX   MEDLINE=97477915; PubMed=9336848;
RA   Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA   Starovasnik M.A.;
RT   "1H, 13C, and 15N backbone assignment and secondary structure of the
RT   receptor-binding domain of vascular endothelial growth factor.";
RL   Protein Sci. 6:2250-2260(1997).
RN   [23]
RP   STRUCTURE BY NMR OF 137-215.
RX   MEDLINE=98298440; PubMed=9634701;
RA   Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA   Starovasnik M.A.;
RT   "Solution structure of the heparin-binding domain of vascular
RT   endothelial growth factor.";
RL   Structure 6:637-648(1998).
RN   [24]
RP   FUNCTION.
RX   MEDLINE=21320570; PubMed=11427521;
RA   Murphy J.F., Fitzgerald D.J.;
RT   "Vascular endothelial growth factor induces cyclooxygenase-dependent
RT   proliferation of endothelial cells via the VEGF-2 receptor.";
RL   FASEB J. 15:1667-1669(2001).
CC   -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC   endothelial cell growth. It induces endothelial cell
CC   proliferation, promotes cell migration, inhibits apoptosis, and
CC   induces permeabilization of blood vessels. It binds to the
CC   VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC   heparin. Neuropilin-1 binds isoforms VEGF-165 and VEGF-145.
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC   with PlGF (By similarity).
CC   -!- SUBCELLULAR LOCATION: VEGF121 is acidic and freely secreted.
CC   VEGF165 is more basic, has heparin-binding properties and,
CC   although a signicant proportion remains cell-associated, most is .

Query Match   74.5%; Score 41; DB 1; Length 232;
Best Local Similarity   66.7%; Pred. No. 2.3;
Matches   6; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
            |||:|||:|
Db   86 CCNDEGLEC 94

```
RESULT 14
VG13_HSVI1
ID   VG13_HSVI1     STANDARD;      PRT;    82 AA.
AC   Q00166;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hypothetical gene 13 zinc-binding protein.
GN   13.
OS   Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Ictalurid Herpes-like viruses.
OX   NCBI_TaxID=10401;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Auburn 1;
RX   MEDLINE=92087490; PubMed=1727613;
RA   Davison A.J.;
RT   "Channel catfish virus: a new type of herpesvirus.";
RL   Virology 186:9-14(1992).
```

```
DR   EMBL; M75136; AAA88194.1; -.
DR   EMBL; M75136; AAA88116.1; -.
DR   PIR; E36787; E36787.
KW   Hypothetical protein; Zinc; Zinc-finger.
SQ   SEQUENCE   82 AA;   8821 MW;   6C009A50FF8C4C67 CRC64;

Query Match             72.7%;   Score 40;  DB 1;  Length 82;
Best Local Similarity   66.7%;   Pred. No. 1.2;
Matches    6;  Conservative   1;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      1  CCNEESLIC 9
           || ||:||:|
Db     11  CCNPMSLIC 19
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RESULT 15
VEGC_RAT
ID   VEGC_RAT     STANDARD;      PRT;    126 AA.
AC   O35757;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Vascular endothelial growth factor C precursor (VEGF-C) (Vascular
DE   endothelial growth factor C related protein) (VRP) (Flt4 ligand) (Flt4-
DE   L) (Fragment).
GN   VEGFC.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Lung;
RA   Mandriota S.J., Pepper M.S.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Growth factor active in angiogenesis, and endothelial
CC       cell growth, stimulating their proliferation and migration and
CC       also has effects on the permeability of blood vessels. May
CC       function in angiogenesis of the venous and lymphatic vascular
CC       systems during embryogenesis, and also in the maintenance of
CC       differentiated lymphatic endothelium in adults. Binds and
CC       activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC   -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC       variety of processed secreted forms with increased activity toward
CC       VEGFR-3, but only the fully processed form could activate VEGFR-2.
CC       VEGF-C first form an antiparallel homodimer linked by disulfide
CC       bonds. Before secretion, a cleavage occurs between arg-227 and
CC       ser-228 producing an heterotetramer. The next extracellular step
CC       of the processing removes the N-terminal propeptide. Finally the
CC       mature VEGF-C is composed mostly of two VEGF homology domains
CC       (VHDs) bound by non-covalent interactions (By similarity).
CC   -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
```

```
DR   EMBL; AF010302; AAB63248.1; -.
DR   HSSP; P15692; 2VPF.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Angiogenesis; Mitogen; Growth factor; Glycoprotein;
KW   Cleavage on pair of basic residues; Multigene family.
FT   NON_TER        1      1
FT   CHAIN          1     71       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT   PROPEP        72   >126       POTENTIAL.
FT   DISULFID       6     53       BY SIMILARITY.
FT   DISULFID      10     55       BY SIMILARITY.
FT   DISULFID      19      9       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD      19     19       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      49     49       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      84     84       N-LINKED (GLCNAC...) (POTENTIAL).
FT   NON_TER      126    126
SQ   SEQUENCE   126 AA;   13977 MW;   8F365AFBC4E037B0 CRC64;

Query Match             70.9%;   Score 39;  DB 1;  Length 126;
Best Local Similarity   66.7%;   Pred. No. 2.8;
Matches    6;  Conservative   0;  Mismatches   0;  Indels   3;  Gaps   0;

Qy      1  CCNEESLIC 9
                     9
Db      9  CCNSEGLQC 17

Search completed: September  5, 2004, 09:56:05
Job time : 4.09091 secs
```

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OM protein - protein search, using sw model

Copyright   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: September 5, 2004, 09:46:09 ; Search time 20.3636 Seconds
          (without alignments)
          139.448 Million cell updates/sec

Title: US-09-761-636A-9
Perfect score: 55
Sequence: 1 CCNEESLIC 9
Scoring table: BLOSUM62
          Gapop 10.0 , Gapext 0.5
Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
          Maximum Match 100%
          Listing first 45 summaries

Database : SPTREMBL_25:*
     1: sp_archea:*
     2: sp_bacteria:*
     3: sp_fungi:*
     4: sp_human:*
     5: sp_invertebrate:*
     6: sp_mammal:*
     7: sp_mhc:*
     8: sp_organelle:*
     9: sp_phage:*
    10: sp_plant:*
    11: sp_rodent:*
    12: sp_virus:*
    13: sp_vertebrate:*
    14: sp_unclassified:*
    15: sp_virus:*
    16: sp_bacteriap:*
    17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	89.1	252	13	Q8QGD7	Q8qgd7 gallus gall
2	49	89.1	326	11	Q91ZE4	Q91ze4 rattus norv
3	46	83.6	152	12	Q8B571	Q8b571 pseudocowpo
4	45	81.8	65	6	Q8MIN0	Q8min0 capra hircu
5	45	81.8	68	6	O97500	O97500 oryctolagus
6	45	81.8	75	6	O18843	O18843 oryctolagus
7	45	81.8	78	6	Q9N1S2	Q9n1s2 capreolus c
8	45	81.8	109	6	Q8MIN1	Q8min1 capra hircu
9	45	81.8	118	6	Q9MZB1	Q9mzb1 ovis aries
10	45	81.8	120	6	Q866G4	Q866g4 oryctolagus
11	45	81.8	123	6	Q9N1S1	Q9n1s1 capreolus c
12	45	81.8	131	6	Q8MJ86	Q8mj86 capreolus c
13	45	81.8	132	12	Q9YMF3	Q9ymf3 orf virus.
14	45	81.8	136	12	Q80GE8	Q80ge8 orf virus.
15	45	81.8	148	13	O42571	O42571 xenopus lae
16	45	81.8	190	6	O77643	O77643 ovis aries
17	45	81.8	194	13	O42572	xenopus lae
18	42	76.4	64	11	Q80UA0	mus musculu
19	42	76.4	110	11	O88911	rattus norv
20	42	76.4	126	3	Q05458	saccharomyc
21	42	76.4	141	11	O70123	mus musculu
22	42	76.4	144	13	O73822	brachydanio
23	42	76.4	188	13	O73682	brachydanio
24	42	76.4	190	11	Q91ZE1	rattus norv
25	41	74.5	190	11	Q9QX39	spalax leuc
26	41	74.5	124	6	Q9GK00	callithrix
27	41	74.5	124	6	Q8SPZ9	sus scrofa
28	41	74.5	126	6	Q9BDP7	macaca mula
29	41	74.5	127	6	Q8WMQ4	sus scrofa
30	41	74.5	128	6	Q8SPL5	equus cabal
31	41	74.5	184	6	Q8HY70	mustela vis
32	41	74.5	189	6	Q95LQ4	felis silve
33	41	74.5	191	4	Q96KJ0	homo sapien
34	41	74.5	191	6	Q96L82	homo sapien
35	41	74.5	191	6	Q95NE5	macaca fasc
36	40	72.7	895	3	Q9C1S1	candida gla
37	39	70.9	146	13	Q90X23	bothrops ja
38	39	70.9	146	13	Q90X24	bothrops in
39	39	70.9	162	10	O82617	arabidopsis
40	39	70.9	326	11	Q91ZH6	meriones un
41	39	70.9	396	13	Q7T3I6	brachydanio
42	39	70.9	415	11	Q91ZE3	rattus norv
43	39	70.9	418	13	O57352	rattus norv
44	38	69.1	316	17	Q8TWK6	methanopyru
45	38	69.1	324	16	Q7V4L6	prochloroco

ALIGNMENTS

RESULT 1
Q8QGD7
ID   Q8QGD7   PRELIMINARY;   PRT;   252 AA.
AC   Q8QGD7;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor D.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Diaz-Trelles R., Rodriguez-Leon J., Kawakami Y.,
RA   Izpisua-Belmonte J.C.;
RT   "Expression of the chick vascular endothelial growth factor D gene
RT   during limb development.";
RL   Mech. Dev. 0:0-0(2002).
DR   EMBL; AF479650; AAM12733.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE 252 AA; 28767 MW; 643475DAB2E72F27 CRC64;

Query Match   89.1%;   Score 49; DB 13; Length 252;
Best Local Similarity 88.9%;   Pred. No. 0.11;
Matches   8; Conservative   8; Mismatches   0; Indels   1; Gaps   0;

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Qy        1 CCNEESLIC 9
            ||||||||
Db      145 CCNEESLISC 153
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RESULT 2
Q91ZE4
ID   Q91ZE4;   PRELIMINARY;   PRT;   326 AA.
AC   Q91ZE4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   VEGF-D.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,
RA   Pepper M.S., Giannis A., Sleeman J.P.;
RT   "Characterization of indolinones which specifically inhibit VEGF-C-and
RT   VEGF-D-induced activation of VEGFR-3 but not VEGFR-2.";
RL   Eur. J. Biochem. 0:0-0(2001).
DR   EMBL; AY032728; AAK96008.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR004153; CXCXC_repeat.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF03128; CXCXC; 1.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   326 AA; 37106 MW; D7CABBA6C9FABB7D CRC64;

Query Match   89.1%; Score 49; DB 11; Length 326;
Best Local Similarity   77.8%; Pred. No. 0.13;
Matches   7; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
            |||||||::|
Db   150 CCNEESVMC 158

RESULT 3
Q8B571
ID   Q8B571;   PRELIMINARY;   PRT;   152 AA.
AC   Q8B571;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vascular endothelial growth factor-like protein.
GN   VEGF.
OS   Pseudocowpox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=129726;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VR634;
RA   Ueda N., Wise L.M., Stacker S.A., Fleming S.B., Mercer A.A.;
RT   "Pseudocowpox virus encodes a homolog of vascular endothelial growth
RT   factor.";
RL   Virology 0:0-0(2003).
DR   EMBL; AF542070; AAO16216.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.

DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   152 AA; 16202 MW; F4B3956D60B37A3D CRC64;

Query Match   83.6%; Score 46; DB 12; Length 152;
Best Local Similarity   77.8%; Pred. No. 0.26;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
            |||:||:||
Db   88 CCNDESQIC 96

RESULT 4
Q8MIN0
ID   Q8MIN0;   PRELIMINARY;   PRT;   65 AA.
AC   Q8MIN0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor 121 (Fragment).
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Corpus luteum;
RA   Kawate N., Tsuji M., Tamada H., Inaba T., Sawada T.;
RT   "Changes of Messenger RNAs Encoding Vascular Endothelial Growth Factor
RT   and Its Receptors during the Development and Maintenance of Caprine
RT   Corpora Lutea.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY114353; AAM76674.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER   1   1
SQ   SEQUENCE   65 AA;   7562 MW; BA3E53B4364B05E3 CRC64;

Query Match   81.8%; Score 45; DB 6; Length 65;
Best Local Similarity   77.8%; Pred. No. 0.19;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
            |||:|||:|
Db   4 CCNDESLEC 12

RESULT 5
O97500
ID   O97500;   PRELIMINARY;   PRT;   68 AA.
AC   O97500;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor (Fragment).
GN   VEGF.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Inoue K., Kawabe Y., Kodama T.;
RT   "Rabbit VEGF cDNA,partial.";

```
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB020216; BAA36949.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER        1       1
FT   NON_TER       68      68
SQ   SEQUENCE   68 AA;   7819 MW;   68763B6661B98DEE0 CRC64;

Query Match             81.8%;   Score 45;   DB 6;   Length 68;
Best Local Similarity   77.8%;   Pred. No. 0.2;
Matches    7;   Conservative    1;   Mismatches    1;   Indels    1;   Gaps    0;

Qy       1 CCNEESLIC 9
           ||:||:|||
Db      40 CCNDESLEC 48

RESULT 6
O18843
ID   O18843      PRELIMINARY;     PRT;    75 AA.
AC   O18843;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor (Fragment).
GN   VEGF.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NEW ZEALAND WHITE; TISSUE=Skeletal muscle;
RX   MEDLINE=98191144; PubMed=9530113;
RA   Skorjanc D., Jaschinski F., Heine G., Pette D.;
RT   "Sequential increases in capillarization and mitochondrial enzymes in
RT   low-frequency-stimulated rabbit muscle.";
RL   Am. J. Physiol. 274:C810-C818(1998).
DR   EMBL; AF022179; AAC15469.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER        1       1
FT   NON_TER       75      75
SQ   SEQUENCE   75 AA;   8720 MW;   DDCE2C5B29E69359 CRC64;

Query Match             81.8%;   Score 45;   DB 6;   Length 75;
Best Local Similarity   77.8%;   Pred. No. 0.22;
Matches    7;   Conservative    1;   Mismatches    1;   Indels    1;   Gaps    0;

Qy       1 CCNEESLIC 9
           ||:||:|||
Db      28 CCNDESLEC 36

RESULT 7


Q9N1S2
ID   Q9N1S2      PRELIMINARY;     PRT;    78 AA.
AC   Q9N1S2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor isoform 121 (Fragment).
GN   VEGF.
OS   Capreolus capreolus (Roe deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Capreolus.
OX   NCBI_TaxID=9858;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=20532861; PubMed=11078967;
RA   Wagener A., Blottner S., Goritz F., Fickel J.;
RT   "Detection of growth factors in the testis of roe deer (Capreolus
RT   capreolus).";
RL   Anim. Reprod. Sci. 64:65-75(2000).
DR   EMBL; AF152593; AAF73232.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   InterPro; IPR002400; GF_cysknot.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER        1       1
FT   NON_TER       78      78
SQ   SEQUENCE   78 AA;   9131 MW;   7EE20DDFFC17847C CRC64;

Query Match             81.8%;   Score 45;   DB 6;   Length 78;
Best Local Similarity   77.8%;   Pred. No. 0.22;
Matches    7;   Conservative    1;   Mismatches    1;   Indels    1;   Gaps    0;

Qy       1 CCNEESLIC 9
           ||:||:|||
Db      24 CCNDESLEC 32

RESULT 8
Q8MIN1
ID   Q8MIN1      PRELIMINARY;     PRT;    109 AA.
AC   Q8MIN1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelila growth factor 165 (Fragment).
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Corpus luteum;
RA   Kawate N., Tsuji M., Tamada H., Inaba T., Sawada T.;
RT   "Changes of Messenger RNAs Encoding Vascular Endothelial Growth Factor
RT   and its Receptors during the Development and Maintenance of Caprine
RT   Corpora Lutea.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY114352; AAM76673.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
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DR    Pfam; PF00341; PDGF; 1.
DR    ProDom; PD001629; PD_growth_factor; 1.
DR    SMART; SM00141; PDGF; 1.
DR    PROSITE; PS50278; PDGF_2; 1.
FT    NON_TER       1      1
SQ    SEQUENCE   109 AA;  12656 MW;  9126572S1A37E023 CRC64;

Query Match             81.8%;  Score 45;  DB 6;  Length 109;
Best Local Similarity   77.8%;  Pred. No. 0.3;
Matches    7;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy       1  CCNEESLIC  9
            |||:||| |
Db       4  CCNDESLEC  12

RESULT 9
Q9MZB1
ID    Q9MZB1     PRELIMINARY;     PRT;   118 AA.
AC    Q9MZB1;
DT    01-OCT-2000 (TrEMBLrel. 15, Created)
DT    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE    Vascular endothelial growth factor (Fragment).
GN    VEGF.
OS    Ovis aries (Sheep).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC    Bovidae; Caprinae; Ovis.
OX    NCBI_TaxID=9940;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Placental artery endothelium;
RA    Zheng J., Tsoi S.C., Magness R.R.;
RT    "Growth factor expression in ovine fetal placental artery endothelial
RT    cells.";
RL    Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AF250375; AAF75258.1; -.
DR    HSSP; P49763; 1FZV.
DR    GO; GO:0016020; C:membrane; IEA.
DR    GO; GO:0008083; F:growth factor activity; IEA.
DR    GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR    InterPro; IPR002400; GF_cysknot.
DR    InterPro; IPR000072; PD_growth_factor.
DR    Pfam; PF00341; PDGF; 1.
DR    PRINTS; PR00438; GFCYSKNOT.
DR    ProDom; PD001629; PD_growth_factor; 1.
DR    SMART; SM00141; PDGF; 1.
DR    PROSITE; PS00249; PDGF_1; 1.
DR    PROSITE; PS50278; PDGF_2; 1.
FT    NON_TER       1      1
SQ    SEQUENCE   118 AA;  13931 MW;  757DC53AA56378A6 CRC64;

Query Match             81.8%;  Score 45;  DB 6;  Length 118;
Best Local Similarity   77.8%;  Pred. No. 0.33;
Matches    7;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy       1  CCNEESLIC  9
            |||:||| |
Db      57  CCNDESLEC  65

RESULT 10
Q866G4
ID    Q866G4     PRELIMINARY;     PRT;   120 AA.
AC    Q866G4;
DT    01-JUN-2003 (TrEMBLrel. 24, Created)
DT    01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE    Vascular endothelial growth factor (Fragment).
GN    VEGF.
OS    Oryctolagus cuniculus (Rabbit).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC    Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX    NCBI_TaxID=9986;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Clausen I., Kietz S., Fischer B.;
RT    "Transcriptional changes in rabbit preimplantation blastocysts upon
RT    exposure to polychlorinated biphenyls.";
RL    Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AY196796; AAO42518.1; -.
DR    GO; GO:0016020; C:membrane; IEA.
DR    GO; GO:0008083; F:growth factor activity; IEA.
DR    GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR    InterPro; IPR002400; GF_cysknot.
DR    InterPro; IPR000072; PD_growth_factor.
DR    Pfam; PF00341; PDGF; 1.
DR    PRINTS; PR00438; GFCYSKNOT.
DR    ProDom; PD001629; PD_growth_factor; 1.
DR    SMART; SM00141; PDGF; 1.
DR    PROSITE; PS00249; PDGF_1; 1.
DR    PROSITE; PS50278; PDGF_2; 1.
FT    NON_TER       1      1
FT    NON_TER     120    120
SQ    SEQUENCE   120 AA;  14032 MW;  E563C54980DCE1E8 CRC64;

Query Match             81.8%;  Score 45;  DB 6;  Length 120;
Best Local Similarity   77.8%;  Pred. No. 0.33;
Matches    7;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy       1  CCNEESLIC  9
            |||:||| |
Db      73  CCNDESLEC  81

RESULT 11
Q9N1S1
ID    Q9N1S1     PRELIMINARY;     PRT;   123 AA.
AC    Q9N1S1;
DT    01-OCT-2000 (TrEMBLrel. 15, Created)
DT    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE    Vascular endothelial growth factor isoform 165 (Fragment).
GN    VEGF.
OS    Capreolus capreolus (Roe deer).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC    Cervidae; Odocoileinae; Capreolus.
OX    NCBI_TaxID=9858;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Testis;
RX    MEDLINE=20532861; PubMed=11078967;
RA    Wagener A., Blottner S., Goritz F., Fickel J.;
RT    "Detection of growth factors in the testis of roe deer (Capreolus
RT    capreolus).";
RL    Anim. Reprod. Sci. 64:65-75(2000).
DR    EMBL; AF152594; AAF73233.1; -.
DR    HSSP; P49763; 1FZV.
DR    GO; GO:0016020; C:membrane; IEA.
DR    GO; GO:0008083; F:growth factor activity; IEA.
DR    GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR    InterPro; IPR002400; GF_cysknot.
DR    InterPro; IPR000072; PD_growth_factor.
DR    Pfam; PF00341; PDGF; 1.
DR    PRINTS; PR00438; GFCYSKNOT.
DR    ProDom; PD001629; PD_growth_factor; 1.
DR    SMART; SM00141; PDGF; 1.
DR    PROSITE; PS00249; PDGF_1; 1.
DR    PROSITE; PS50278; PDGF_2; 1.
FT    NON_TER       1      1
FT    NON_TER     123    123
SQ    SEQUENCE   123 AA;  14354 MW;  0A756F54105A4CE1 CRC64;

Query Match             81.8%;  Score 45;  DB 6;  Length 123;
```

```
Best Local Similarity  77.8%;  Pred. No. 0.34;
Matches    7;  Conservative   1;  Mismatches   1;  Indels    0;  Gaps    0;

Qy         1  CCNEESLIC  9
              |||:|||| |
Db        24  CCNDESLEC 32

RESULT 12
Q8MJ86
ID   Q8MJ86       PRELIMINARY;      PRT;    131 AA.
AC   Q8MJ86;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor-3 (Fragment).
OS   Capreolus capreolus (Roe deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Capreolus.
OX   NCBI_TaxID=9858;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Wagener A., Fickel J.;
RT   "Detection of VEGF in roe deer testis.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF514284; AAM49789.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     131    131
SQ   SEQUENCE   131 AA;  15358 MW;  99719A58BEAC7FCA CRC64;

Query Match             81.8%;  Score 45;  DB 6;  Length 131;
Best Local Similarity   77.8%;  Pred. No. 0.36;
Matches    7;  Conservative   1;  Mismatches   1;  Indels    0;  Gaps    0;

Qy         1  CCNEESLIC  9
              |||:|||| |
Db         2  CCNDESLEC 10

RESULT 13
Q9YMF3
ID   Q9YMF3       PRELIMINARY;      PRT;    132 AA.
AC   Q9YMF3;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor homolog Vegf-e (Vascular
DE   endothelial growth factor-like protein).
GN   VEGF-E.
OS   Orf virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=10258;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=D1701;
RX   MEDLINE=99107753; PubMed=9889193;
RA   Meyer M., Clauss M., Lepple-Wienhues A., Waltenberger J.,
RA   Augustin H.G., Ziche M., Lanz C., Buettner M., Rziha H.J., Dehio C.;
RT   "A novel vascular endothelial growth factor encoded by orf virus,
RT   VEGF-E, mediates angiogenesis via signalling through VEGFR-2 (KDR) but
RT   not VEGFR-1 (Flt-1) receptor tyrosine kinases.";
RL   EMBO J. 18:363-374(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=D1701;
RX   PubMed=12692275;
RA   Rziha H.-J., Bauer B., Adam K.-H., Rottgen M., Cottone R., Henkel M.,
RA   Dehio C., Buttner M.;
RT   "Relatedness and heterogeneity at the near-terminal end of the genome
RT   of a parapoxvirus bovis 1 strain (B177) compared with parapoxvirus
RT   ovis (Orf virus).";
RL   J. Gen. Virol. 84:1111-1116(2003).
DR   EMBL; AF106020; AAD03735.1; -.
DR   EMBL; AY186732; AAO31702.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_Cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   132 AA;  14763 MW;  15F403A068B72926 CRC64;

Query Match             81.8%;  Score 45;  DB 12;  Length 132;
Best Local Similarity   77.8%;  Pred. No. 0.36;
Matches    7;  Conservative   1;  Mismatches   1;  Indels    0;  Gaps    0;

Qy         1  CCNEESLIC  9
              |||:|||| |
Db        69  CCNDESLEC 77

RESULT 14
Q80GE8
ID   Q80GE8       PRELIMINARY;      PRT;    136 AA.
AC   Q80GE8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VEGF-like protein.
OS   Orf virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Parapoxvirus.
OX   NCBI_TaxID=10258;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Orf-11;
RA   McInnes C.J., Wood A.R.;
RT   "A preliminary transcript map of the early genes of orf virus.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY236150; AAP03726.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_Cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   136 AA;  15082 MW;  9768C9C42E6CB267 CRC64;

Query Match             81.8%;  Score 45;  DB 12;  Length 136;
Best Local Similarity   77.8%;  Pred. No. 0.37;
Matches    7;  Conservative   1;  Mismatches   1;  Indels    0;  Gaps    0;

Qy         1  CCNEESLIC  9
              |||:|||| |
```

Db   70 CCNDESLEC 78

RESULT 15
O42571
ID   O42571   PRELIMINARY;   PRT;   148 AA.
AC   O42571;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vascular endothelial growth factor 122.
GN   VEGF.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
RT   "Neovascularization of the Xenopus embryo.";
RL   Dev. Dyn. 0:0-0(1997).
DR   EMBL; AF008593; AAB63679.1; -.
DR   HSSP; P49763; 1FZV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PD_growth_factor.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PD_growth_factor; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE 148 AA; 17234 MW; 4AD153CA2F8B1B95 CRC64;

Query Match   81.8%; Score 45; DB 13; Length 148;
Best Local Similarity   77.8%; Pred. No. 0.4;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
            ||| | |||
Db   86 CCNDESLEC 94

Search completed: September 5, 2004, 09:59:59
Job time : 21.3636 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:37:49 ; Search time 29.5455 Seconds
              (without alignments)
              86.068 Million cell updates/sec

Title: US-09-761-636A-9
Perfect score: 55
Sequence: 1 CCNEESLIC 9
Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_29Jan04:*
              1: geneseqp1980s:*
              2: geneseqp1990s:*
              3: geneseqp2000s:*
              4: geneseqp2001s:*
              5: geneseqp2002s:*
              6: geneseqp2003as:*
              7: geneseqp2003bs:*
              8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	9	4	AAU04528	Aau04528 VEGF base
2	55	100.0	73	4	AAU04522	Aau04522 Human VEG
3	55	100.0	96	4	AAU04520	Aau04520 Human VEG
4	55	100.0	109	2	AAY23889	Aay23889 Human vas
5	55	100.0	109	6	AAB11931	Aab11931 Human tru
6	55	100.0	109	6	ABB84621	Abb84621 Human wil
7	55	100.0	287	6	ABG73779	Abg73779 Human NVR
8	55	100.0	325	2	AAW53240	Aaw53240 Homo sapi
9	55	100.0	325	4	AAY97572	Aay97572 Human VEG
10	55	100.0	354	2	AAW44293	Aaw44293 Human vas
11	55	100.0	354	2	AAW49036	Aaw49036 Human zve
12	55	100.0	354	2	AAW53241	Aaw53241 Homo sapi
13	55	100.0	354	3	AAB10649	Aab10649 Human VEG
14	55	100.0	354	3	AAY70750	Aay70750 Human pre
15	55	100.0	354	3	AAY70983	Aay70983 Human vas
16	55	100.0	354	3	AAB29049	Aab29049 Human VEG
17	55	100.0	354	4	AAB37606	Aab37606 Human VEG
18	55	100.0	354	4	AAY97573	Aay97573 Human VEG
19	55	100.0	354	4	AAU08441	Aau08441 Polypepti
20	55	100.0	354	5	ABG33055	Abg33055 Human vas
21	55	100.0	354	5	ABG32046	Abg32046 Human Flt
22	55	100.0	354	6	ABB84623	Abb84623 Human VEG
23	55	100.0	354	7	ADD08950	Add08950 Human VEG
24	50	90.9	9	4	AAU04552	Aau04552 VEGF base
25	50	90.9	109	6	ABG73750	Abg73750 Human VEG
26	49	89.1	9	4	AAU04553	Aau04553 VEGF base
27	49	89.1	326	2	AAW44296	Aaw44296 Rat vascu
28	48	87.3	354	4	AAB70685	Aab70685 Human vas
29	48	87.3	620	2	AAW14994	Aaw14994 Human c-F
30	46	83.6	8	4	AAU04525	Aau04525 VEGF base
31	45	81.8	101	2	AAW86229	Aaw86229 Poxvirus
32	45	81.8	106	2	AAW86228	Aaw86228 Poxvirus
33	45	81.8	110	5	AAM47933	Aam47933 Mouse VEG
34	45	81.8	111	2	AAW86227	Aaw86227 Poxvirus
35	45	81.8	116	2	AAW86226	Aaw86226 Poxvirus
36	45	81.8	120	2	AAR10916	Aar10916 Bovine va
37	45	81.8	120	2	AAR38916	Aar38916 Bovine VE
38	45	81.8	132	2	AAW40305	Aaw40305 Parapox v
39	45	81.8	132	2	AAY33434	Aay33434 Parapox v
40	45	81.8	132	3	AAY92776	Aay92776 Orf virus
41	45	81.8	132	4	AAY97574	Aay97574 Human VEG
42	45	81.8	132	4	AAU08466	Aau08466 Polypepti
43	45	81.8	133	2	AAY33443	Aay33443 Parapox v
44	45	81.8	133	2	AAY33435	Aay33435 Parapox v
45	45	81.8	133	2	AAW86206	Aaw86206 Poxvirus

ALIGNMENTS

RESULT 1
AAU04528
ID   AAU04528 standard; protein; 9 AA.
XX
AC   AAU04528;
XX
DT   26-SEP-2001 (first entry)
XX
DE   VEGF based bicyclic dimeric peptide #2.
XX
KW   Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation; cyclic.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Disulfide-bond 1
FT   /note= "A disulfide bond forms between residue 1 and
FT   residue 1 of an identical peptide to form a dimeric
FT   peptide, or between residue 1 and residue 17 of the
FT   sequence appearing as AAU04527 also forming a dimeric
FT   peptide"
FT   Disulfide-bond 2..9
FT   /note= "This bond cyclises the peptide"
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-44248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Claim 59; Page 32; 102pp; English.

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XX
CC   The sequence represents a dimeric bicyclic peptide of the invention,
CC   whose 3-dimensional structure is modelled on the expose loop of human
CC   VEGFD (vascular endothelial growth factor). The invention relates to a
CC   method of producing a monomeric monocyclic peptide by a measuring beta-
CC   beta carbon separation distances on opposite antiparallel strands of a
CC   peptide loop fragment from an exposed loop of a growth factor protein and
CC   cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC   peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC   peptides) and a cyclic peptide with at least one amino acid deleted prior
CC   to cyclisation are used to interfere with angiogenesis,
CC   neovascularisation or lymphangiogenesis in a mammal with a condition
CC   characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC   The condition is diabetic retinopathy, psoriasis, arthropathy,
CC   hemangioma, vascularised malignant or benign tumour, post-recovery
CC   cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC   trauma, substance-induced neovascularisation of the liver, excessive
CC   hormone-related angiogenic dysfunction, diabetes induced neovascular
CC   sequelae, hypertension induced neovascular sequelae, or chronic liver
CC   infection. The peptides are also used to modulate vascular permeability
CC   in a mammal (the mammal has a condition characterised by fluid
CC   accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC   or brain. The peptides are used to image blood vessels and lymphatic
CC   vasculature. The monomeric and bicyclic peptides are used to interfere
CC   with at least one biological activity induced by VEGF, VEGF-C or -D and
CC   are also used in combination with an anti-inflammatory agent, to treat a
CC   chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC   diabetic retinopathy
XX
SQ   Sequence 9 AA;

Qy        1  CCNEESLIC 9
             |||||||||
Db        1  CCNEESLIC 9

Query Match           100.0%;  Score 55;  DB 4;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 1.4e+06;
Matches      9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT 2
AAU04522
ID   AAU04522 standard; protein; 73 AA.
XX
AC   AAU04522;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human VEGF-D amino acids Val101-Thr 173.
XX
KW   Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 1; Page 90-91; 102pp; English.
XX
CC   The sequence represents Human VEGF-D (vascular endothelial growth factor)
CC   amino acids Val101-Thr 173, used together with the C-terminal 23 residues
CC   of VEGF to make a hybrid theoretical molecule for 3 dimensional
CC   modelling. The sequence is used in a method of producing a monomeric
CC   monocyclic peptide by a measuring beta-beta carbon separation distances
CC   on opposite antiparallel strands of a peptide loop fragment from an
CC   exposed loop of a growth factor protein and cyclising the peptide by
CC   oxidising the cysteine residues. The monocyclic peptides, dimeric
CC   bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
CC   peptide with at least one amino acid deleted prior to cyclisation are
CC   used to interfere with angiogenesis, neovascularisation or
CC   lymphangiogenesis in a mammal with a condition characterised by
CC   angiogenesis, neovascularisation or lymphangiogenesis. The condition is
CC   diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
CC   malignant or benign tumour, post-recovery cerebrovascular accident, post-
CC   angioplasty restenosis, head, heat or cold trauma, substance-induced
CC   neovascularisation of the liver, excessive hormone-related angiogenic
CC   dysfunction, diabetes induced neovascular sequelae, hypertension induced
CC   neovascular sequelae, or chronic liver infection. The peptides are also
CC   used to modulate vascular permeability in a mammal (the mammal has a
CC   condition characterised by fluid accumulation in peripheral limbs or in
CC   lungs, peritoneal cavity, pleura, or brain. The peptides are used to
CC   image blood vessels and lymphatic vasculature. The monomeric and bicyclic
CC   peptides are used to interfere with at least one biological activity
CC   induced by VEGF, VEGF-C or -D and are also used in combination with an
CC   anti-inflammatory agent, to treat a chronic inflammation, especially
CC   rheumatoid arthritis, psoriasis and diabetic retinopathy
XX
SQ   Sequence 73 AA;

Query Match           100.0%;  Score 55;  DB 4;  Length 73;
Best Local Similarity 100.0%;  Pred. No. 0.44;
Matches      9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1  CCNEESLIC 9
             |||||||||
Db       45  CCNEESLIC 53

RESULT 3
AAU04520
ID   AAU04520 standard; protein; 96 AA.
XX
AC   AAU04520;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human VEGF-D amino acids Val101-PRO186.
XX
KW   Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
KW   neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW   diabetes induced neovascular sequelae; rheumatoid arthritis;
KW   diabetic retinopathy; chronic inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200152875-A1.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001533.
XX
PR   18-JAN-2000; 2000US-0176293P.
PR   16-MAY-2000; 2000US-0204590P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
```

```
PI   Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR   WPI; 2001-442248/47.
XX
PT   Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT   or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT   from an exposed loop of a growth factor protein by oxidizing the cysteine
PT   residues.
XX
PS   Example 1; Page 89; 102pp; English.
XX
CC   The sequence represents Human VEGF-D (vascular endothelial growth factor)
CC   amino acids Val101-PRO186. The sequence is used in a method of producing
CC   a monomeric monocyclic peptide by a measuring beta-beta carbon separation
CC   distances on opposite antiparallel strands of a peptide loop fragment
CC   from an exposed loop of a growth factor protein and cycling the peptide
CC   by oxidising the cysteine residues. The monocyclic peptides; dimeric
CC   bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
CC   peptide with at least one amino acid deleted prior to cyclisation are
CC   used to interfere with angiogenesis, neovascularisation or
CC   lymphangiogenesis in a mammal with a condition characterised by
CC   angiogenesis, neovascularisation or lymphangiogenesis. The condition is
CC   diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
CC   malignant or benign tumour, post-recovery cerebrovascular accident, post-
CC   angioplasty-restenosis, head, heat or cold trauma, substance-induced
CC   neovascularisation of the liver, excessive hormone-related angiogenic
CC   dysfunction, diabetes induced neovascular sequelae, hypertension induced
CC   neovascular sequelae, or chronic liver infection. The peptides are also
CC   used to modulate vascular permeability in a mammal (the mammal has a
CC   condition characterised by fluid accumulation in peripheral limbs or in
CC   lungs, peritoneal cavity, pleura, or brain. The peptides are used to
CC   image blood vessels and lymphatic vasculature. The monomeric and bicyclic
CC   peptides are used to interfere with at least one biological activity
CC   induced by VEGF, VEGF-C or -D and are also used in combination with an
CC   anti-inflammatory agent, to treat a chronic inflammation, especially
CC   rheumatoid arthritis, psoriasis and diabetic retinopathy.
XX
SQ   Sequence 96 AA;

Query Match             100.0%;  Score 55;  DB 4;  Length 96;
Best Local Similarity   100.0%;  Pred. No. 0.57;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1  CCNEESLIC  9
             |||||||||
Db       45  CCNEESLIC  53

RESULT 4
AAY23889
ID   AAY23889 standard; protein; 109 AA.
XX
AC   AAY23889;
XX
DT   21-SEP-1999  (first entry)
XX
DE   Human vascular endothelial growth factor (VEGF)-D.
XX
KW   Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma;
KW   tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft;
KW   wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.
XX
OS   Homo sapiens.
XX
PN   WO9933485-A1.
XX
PD   08-JUL-1999.
XX
PF   23-DEC-1998;  98WO-US027373.
XX
PR   24-DEC-1997;  97AU-00001131.
PR   29-MAY-1998;  98US-0087392P.
XX


PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Stacker SA, Alitalo K;
XX
DR   WPI; 1999-405368/34.
XX
PT   A human cell line stably expressing vascular endothelial growth factor D,
PT   useful for treating melanomas or tumors expressing VEGF-D.
XX
PS   Claim 6; Page 72; 79pp; English.
XX
CC   The present sequence represents human vascular endothelial growth factor
CC   (VEGF)-D. The specification describes a human cell line which stably
CC   expresses VEGF-D, or fragments/analogues having VEGF-D biological
CC   activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex
CC   DNA, VEGF-D variants or antibodies (especially chimeric antibodies), are
CC   useful for the treatment or alleviation of malignant melanomas, tumours
CC   or psoriasis. Angiogenesis and lymphangiogenesis stimulating amounts of
CC   VEGF-D can be administered to enhance the acceptance and/or healing of
CC   skin grafts or to stimulate the healing of a surgical or traumatic wound
CC   to the skin. Lymphangiogenesis stimulating amounts of VEGF-D can be used
CC   to treat lymphedema. Endothelial proliferation stimulating amounts of
CC   VEGF-D are used to treat scleroderma. Vascularisation stimulating amounts
CC   of VEGF-D can be used to treat anhydrotic ectodermal dysplasia. VEGF-D
CC   antibodies are useful for detecting tumours expressing VEGF-D. Fully-
CC   processed VEGF-D can be used to stimulate at least one VEGF-D bioactivity
CC   chosen from endothelial cell proliferation, migration, survival and
CC   differentiation and lymphangiogenesis without inducing vascular
CC   permeability
XX
SQ   Sequence 109 AA;

Query Match             100.0%;  Score 55;  DB 2;  Length 109;
Best Local Similarity   100.0%;  Pred. No. 0.63;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1  CCNEESLIC  9
             |||||||||
Db       53  CCNEESLIC  61

RESULT 5
AAB11931
ID   AAB11931 standard; protein; 109 AA.
XX
AC   AAB11931;
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human truncated VEGF-D.
XX
KW   Truncated VEGF-D; vascular endothelial growth factor; human;
KW   monoclonal antibody; VEGF receptor; VEGFR-2; VEGFR-3;
KW   vascular permeability disorder; endothelial cell proliferative disorder;
KW   angiogenic disorder; lymphangiogenic disorder;
KW   neovascularisation disorder; endothelial cell differentiation disorder;
KW   cancer; diabetic retinopathy; psoriasis; arthropathy; pulmonary oedema;
KW   detection; diagnosis; imaging; lymphatic vasculature.
XX
OS   Homo sapiens.
XX
PN   WO20003T025-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;  99WO-US031332.
XX
PR   21-DEC-1998;  98US-0113254P.
PR   17-MAY-1999;  99US-0134556P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Achen MG, Stacker SA;
```

XX
DR   WPI; 2000-442498/38.
XX
PT   Novel compositions comprising antibodies reactive to vascular endothelial
PT   growth factor-D, useful for treating, e.g. angiogenesis, lymphogiogenesis
PT   and neovascularization disorders.
XX
PS   Claim 1; Fig 1; 44pp; English.
XX
CC   This sequence represents a 109 amino acid truncated human VEGF-D
CC   (vascular endothelial growth factor D), lacking both the N- and C-
CC   terminal regions. The invention relates to a monoclonal antibody, or
CC   fragments thereof, which is specifically reactive with the truncated
CC   human VEGF-D, and methods of preparing the antibody. The antibody of the
CC   invention interferes with the binding of VEGF-D to the VEGF receptors
CC   VEGFR-2 and VEGFR-3, but does not interfere with the binding of VEGF to
CC   these receptors and additionally is not reactive with VEGF-C. The
CC   antibody may be used to treat disorders associated with vascular
CC   permeability, endothelial cell proliferation, angiogenesis,
CC   lymphangiogenesis, neovascularisation and endothelial cell
CC   differentiation, especially cancer, diabetic retinopathy, psoriasis, and
CC   arthropathies. The antibody may also be used to treat fluid accumulation
CC   in the heart and/or lung via modulation of vascular permeability. It may
CC   additionally be used to detect VEGF-D and may be used to image lymphatic
CC   vasculature in tissue
XX
SQ   Sequence 109 AA;

Query Match   100.0%;   Score 55; DB 3; Length 109;
Best Local Similarity   100.0%;   Pred. No. 0.63;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
         |||||||||
Db   53 CCNEESLIC 61

RESULT 6
ABB84621
ID   ABB84621 standard; protein; 109 AA.
XX
AC   ABB84621;
XX
DT   01-APR-2003 (first entry)
XX
DE   Human wild-type VEGF-D monomer SEQ ID 3.
XX
KW   Human; single-chain; extracellular ligand-binding domain; VEGF;
KW   vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
KW   VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
KW   lymphangiogenesis.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Region   8..18
FT   /note="region of monomer likely to be modified by
FT   mutation as described in claim 9"
FT   Region   36..49
FT   /note="region of monomer likely to be modified by
FT   mutation as described in claim 9"
FT   Region   55..60
FT   /note="region of monomer likely to be modified by
FT   mutation as described in claim 9"
FT   Misc-difference 60
FT   /note="This residues is described as Gln in Claim 9"
FT   Region   70..86
FT   /note="region of monomer likely to be modified by
FT   mutation as described in claim 9"
XX
PN   WO200281520-A2.
XX
PD   17-OCT-2002.

XX
PF   08-APR-2002; 2002WO-DK000233.
XX
PR   06-APR-2001; 2001DK-00000578.
PR   06-APR-2001; 2001US-0282239P.
XX
PA   (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI   Boesen TP, Halkier T;
XX
DR   WPI; 2003-058505/05.
XX
PT   Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds
PT   to extracellular ligand-binding domain of vascular endothelial growth
PT   factor type 2/type 3 receptor but does not activate the receptor.
XX
PS   Claim 9; Page 66; 71pp; English.
XX
CC   This invention describes a novel single-chain dimeric polypeptide which
CC   binds to extracellular ligand-binding domain of vascular endothelial
CC   growth factor (VEGF) type 2 receptor (KDR) or VEGF type 3 receptor (Flt-
CC   4). The polypeptide of the invention comprises two receptor-binding sites
CC   of which one is capable of binding to a ligand-binding domain of the
CC   receptor and one is incapable of effectively binding to a ligand-binding
CC   domain of the receptor, and at least one monomer of the dimeric
CC   polypeptide is derived from VEGF, VEGF-C or VEGF-D, where the polypeptide
CC   is capable of binding to the receptor, but incapable of activating a
CC   receptor. The polypeptide of the invention is useful for preparing a
CC   medicament for preventing or treating a disease or condition involving
CC   increased signal transduction from, or an increased activation of a VEGF
CC   type 2 or type 3 receptor e.g. for inhibiting angiogenesis or
CC   lymphangiogenesis. This sequence represents a human single-chain VEGF-D
CC   monomer which can be modified and used in the construction of a VEGF-
CC   based KDR antagonist described in the disclosure of the invention
XX
SQ   Sequence 109 AA;

Query Match   100.0%;   Score 55; DB 6; Length 109;
Best Local Similarity   100.0%;   Conservative   0; Mismatches   0; Pred. No. 0.63;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
         |||||||||
Db   53 CCNEESLIC 61

RESULT 7
ABG73779
ID   ABG73779 standard; protein; 287 AA.
XX
AC   ABG73779;
XX
DT   03-APR-2003 (first entry)
XX
DE   Human NVR protein.
XX
KW   NVR; human; endothelial growth factor; cytostatic; cancer; angiogenesis;
KW   cell proliferation; revascularisation; amputation; vasculogenesis;
KW   transplant; brain; breast; intestine; kidney; lung; ovary; pancreas;
KW   prostate; uterus; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Misc-difference 281
FT   /note="Encoded by TAA, an in frame stop codon which
FT   interrupts the coding region as shown in Figure 1A-B.
FT   This site is the end of the protein sequence represented
FT   in SEQ ID 1 of the Sequence listing"
FT   Region   282..287
FT   /note="Region not represented in SEQ ID 1 of the
FT   Sequence listing"
XX

PN US2002155538-A1.
XX
PD 24-OCT-2002.
XX
PF 09-JAN-2002; 2002US-00044622.
XX
PR 23-JAN-1997; 97US-00788812.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Goli SK, Murry LE;
XX
DR WPI; 2003-182635/18.
DR N-PSDB; ABQ77105.
XX
PT New endothelial growth factor polypeptide and polynucleotides, useful for
PT diagnosing, preventing, and treating cancer and other conditions or
PT diseases involving angiogenesis and cell proliferation.
XX
PS Claim 1; Fig 1A-B; 28pp; English.
XX
CC This invention describes a novel human endothelial growth factor
CC polypeptide which has cytostatic activity. The polypeptide and its
CC encoding polynucleotide are useful in the diagnosis, prevention, and
CC treatment of cancer and other conditions or diseases involving
CC angiogenesis and cell proliferation. NVR may also be used to promote
CC revascularisation following traumatic amputation and surgical
CC reconstruction or added to a tissue culture to promote vasculogenesis in
CC tissues for autologous or heterologous transplant. Antagonists or
CC inhibitors of NVR may be used to suppress or prevent angiogenesis and
CC thus prevent the growth and development of cancers such as cancer of the
CC brain, breast, intestine, kidney, lung, ovary, pancreas, prostate or
CC uterus. The products of the invention can be used for gene therapy. This
CC sequence represents the human NVR protein described in the disclosure of
CC the invention
XX
SQ Sequence 287 AA;
XX
Query Match 100.0%; Score 55; DB 6; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCNEESLIC 9
|||||||||
Db 145 CCNEESLIC 153

RESULT 8
AAW53240
ID AAW53240 standard; protein; 325 AA.
XX
AC AAW53240;
XX
DT 03-AUG-1998 (first entry)
XX
DE Homo sapiens vascular endothelial growth factor D (VEGF-D).
XX
KW vascular endothelial growth factor; VEGF-D; angiogenesis; modification;
KW acceleration; wound healing; tissue; organ; transplants;
KW collateral circulation; infarction; arterial stenosis;
KW coronary artery disease; inhibition; cancer; treatment;
KW diabetic retinopathy; lung disorders; blood circulation;
KW gaseous exchange; chronic obstructive airway disease;
KW intestinal malabsorptive syndrome; biopsy; metastatic risk; detection;
KW diagnosis; congestive heart failure.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 126..128
FT /note= "potential N-linked glycosylation site"
FT Region 156..158
FT /note= "potential N-linked glycosylation site"
FT Region 258..260
FT /note= "potential N-linked glycosylation site"
XX
PN WO9807832-A1.
XX
PD 26-FEB-1998.
XX
PF 21-AUG-1997; 97WO-US014696.
XX
PR 23-AUG-1996; 96AU-00001825.
PR 23-AUG-1996; 96US-0023751P.
PR 11-NOV-1996; 96AU-00003554.
PR 14-NOV-1996; 96US-0031097P.
PR 05-FEB-1997; 97AU-00004954.
PR 19-JUN-1997; 97US-0038814P.
PR 01-JUL-1997; 97AU-0007435.
PR 97US-0051426P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
PI Achen MG, Wilks AF, Stacker SA, Alitalo K;
XX
DR WPI; 1998-179057/16.
DR N-PSDB; AAV20806.
XX
PT New isolated vascular endothelial growth factor-D - used to develop
PT products for use in e.g. modifying angiogenesis or treating lung, heart
PT or intestinal disorders.
XX
PS Claim 16; Page 57-58; 101pp; English.
XX
CC The sequence is that of human breast vascular endothelial growth factor D
CC (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in
CC wound healing, tissue or organ transplantation, or to establish
CC collateral circulation in tissue infarction or arterial stenosis, such as
CC coronary artery disease, and inhibition of angiogenesis in the treatment
CC of cancer or of diabetic retinopathy. It can also be used in the
CC treatment of lung disorders to improve blood circulation in the lung
CC and/or gaseous exchange between the lungs and the blood stream or to
CC improve blood circulation to the heart and O2 gas permeability in cases
CC of cardiac insufficiency, to improve blood flow and gaseous exchange in
CC chronic obstructive airway disease, or to treat malabsorptive syndromes
CC in the intestinal tract. Quantitation of VEGF-D in cancer biopsy
CC specimens may be useful as an indicator of future metastatic risk.
CC Antagonists can be used for treating e.g. conditions such as congestive
CC heart failure, involving accumulations of fluid in the lung resulting
CC from increases in vascular permeability. The products can also be used
CC for detection and diagnosis
XX
SQ Sequence 325 AA;

Query Match 100.0%; Score 55; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCNEESLIC 9
|||||||||
Db 116 CCNEESLIC 124

RESULT 9
AAY97572
ID AAY97572 standard; protein; 325 AA.
XX
AC AAY97572;
XX
DT 05-APR-2001 (first entry)
XX
DE Human VEGF-D protein sequence.
XX
KW Human; angiogenic protein; wound healing; vascular tissue repair;
KW peripheral arterial disease; critical limb ischaemia; coronary disease;

KW   angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis;
KW   rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
KW   infectious disease; neurodegeneration;
KW   vascular endothelial growth factor-D; VEGF-D.
XX
OS   Homo sapiens.
XX
PN   WO200075163-A1.
XX
PD   14-DEC-2000.
XX
PF   01-JUN-2000; 2000WO-US014925.
XX
PR   03-JUN-1999; 99US-0137796P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Ruben SM, Hu J, Cao L;
XX
DR   WPI; 2001-071057/08.
DR   N-PSDB; AAA91006.
XX
PT   New nucleic acid encoding angiogenic proteins, useful e.g. for promoting
PT   healing of wounds and treating peripheral arterial disease, critical limb
PT   ischemia or coronary disease.
XX
PS   Claim 11; Page 226-227; 244pp; English.
XX
CC   This sequence is vascular endothelial growth factor-D (VEGF-D), which is
CC   an angiogenic protein of the invention. The angiogenic proteins and the
CC   DNA sequences encoding them, are used to prevent, treat or ameliorate
CC   disease and to detect diseases, or susceptibility, by detecting mutations
CC   or the presence or amount of angiogenic protein expression. Particularly
CC   they are used to stimulate wound healing, growth of damaged bone and
CC   tissue, and for repair of vascular tissue, especially peripheral arterial
CC   disease, critical limb ischaemia or coronary disease. Antagonists of the
CC   sequences are used to inhibit angiogenesis in tumours and to treat
CC   inflammation (where associated with increased vascular permeability),
CC   diabetic retinopathy, rheumatoid arthritis or psoriasis. Agonists are also
CC   also useful for stimulating (lymph)angiogenesis. The proteins are also
CC   used to identify specific binding agents (potential therapeutic agents)
CC   and to raise antibodies. The antibodies are useful as therapeutic
CC   (ant)agonists; for detection, purification and targeting of proteins for
CC   in vivo or in vitro diagnosis (including imaging) or for therapy
CC   (including when linked to e.g. a label or cytotoxin); and for
CC   immunotyping of cells, e.g. for detecting minimal residual disease or
CC   haematopoietic progenitor/stem cells. It is also contemplated that the
CC   sequences might be useful for treating a very wide range of other
CC   disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases
CC   (viral, bacterial, fungal or parasitic); neurodegeneration, also as
CC   chemotactic agents or for stimulating regeneration of the nervous system
CC   etc
XX
SQ   Sequence 325 AA;

Query Match   100.0%; Score 55; DB 4; Length 325;
Best Local Similarity   100.0%; Pred. No. 1.7;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
              |||||||||
Db   116 CCNEESLIC 124

RESULT 10
AAW44293
ID   AAW44293 standard; protein; 354 AA.
XX
AC   AAW44293;
XX
DT   22-JUN-1998 (first entry)
XX
DE   Human vascular endothelial growth factor D.

XX
KW   Human; vascular endothelial growth factor D, VEGF-D; gene therapy;
KW   inflammation; oedema.
XX
OS   Homo sapiens.
XX
PN   WO9802543-A1.
XX
PD   22-JAN-1998.
XX
PF   15-JUL-1997;   97WO-JP002456.
XX
PR   15-JUL-1996;   96JP-00185216.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Hirata Y, Nezu J;
XX
DR   WPI; 1998-110591/10.
DR   N-PSDB; AAV15156.
XX
PT   VEGF-D protein encoded by DNA - useful for, e.g. gene therapy and
PT   treating oedema.
XX
PS   Claim 1; Page 18-20; 52pp; Japanese.
XX
CC   The present sequence represents human vascular endothelial growth factor
CC   D (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind
CC   the protein, may be useful in, e.g. gene therapy and in treatment of
CC   inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D
CC   DNA sequences may be used for screening for the compounds which bind to
CC   the VEGF-D protein
XX
SQ   Sequence 354 AA;

Query Match   100.0%; Score 55; DB 2; Length 354;
Best Local Similarity   100.0%; Pred. No. 1.8;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
              |||||||||
Db   145 CCNEESLIC 153

RESULT 11
AAW49036
ID   AAW49036 standard; protein; 354 AA.
XX
AC   AAW49036;
XX
DT   26-OCT-1998 (first entry)
XX
DE   Human zvegf2 growth factor.
XX
KW   Human zvegf2 growth factor; mitogen; fibroblast; smooth muscle cell;
KW   venous stasis ulcer; diabetic ulcer; skin wound; chemotactic effect;
KW   angiogenic effect; tumour; diabetic retinopathy; psoriasis; arthritis;
KW   scleroderma.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..23
FT   /note= "Signal peptide"
FT   Peptide   24..108
FT   /note= "Pro-region"
FT   Binding-site 109..197
FT   /note= "Receptor binding domain"
FT   Region   206..256
FT   /note= "Cysteine-rich domain"
FT   Region   257..274
FT   /note= "Balbiani ring motif"
FT   Region   275..294

FT Region   /note= "Balbiani ring motif"
FT   295..354
FT   /note= "Cysteine-rich domain"
XX
PN WO9824811-A2.
XX
PD 11-JUN-1998.
XX
PF 20-NOV-1997;   97WO-US020888.
XX
PR 06-DEC-1996;   96US-00759657.
PR 18-SEP-1997;   97US-00933455.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gilbert T, Conklin DC, Hart CE, Nygaard S, Sheppard PO;
XX
DR WPI; 1998-333256/29.
DR N-PSDB; AAV32823.
XX
PT New isolated vascular endothelial growth factor - used to develop
PT products for treating e.g. wounds, burns, myocardial infarction, tumours,
PT psoriasis, arthritis, restenosis or organ transplants.
XX
PS Claim 1; Page 53-54; 77pp; English.
XX
CC The present sequence represents a human zvegf2 growth factor encoded by
CC the zvegf2 cDNA which was isolated from a human heart cDNA library.
CC zvegf2 protein in a dimeric form acts as a mitogen for fibroblasts or
CC smooth muscle cells. zvegf2 is claimed to be useful for stimulating the
CC revascularisation of tissue or the re-endothelialisation of vascular
CC tissue. zvegf2 is particularly claimed to be useful for the treatment of
CC full-thickness skin wounds, including venous stasis ulcers and diabetic
CC ulcers. The zvegf2 protein is also claimed to be useful as an additive in
CC tissue adhesives for promoting revascularisation of the healing tissue.
CC Antagonists against zvegf2 can be used to block its mitogenic,
CC chemotactic and angiogenic effects. The antagonists may therefore be
CC useful for reducing growth of solid tumour by inhibiting
CC neovascularisation of the developing tumour or by directly blocking
CC tumour cell growth, in the treatment of diabetic retinopathy, psoriasis,
CC arthritis, and scleroderma
XX
SQ Sequence 354 AA;

Query Match   100.0%;   Score 55; DB 2;   Length 354;
Best Local Similarity 100.0%;   Pred. No. 1.8;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
             |||||||||
Db   145 CCNEESLIC 153

RESULT 12
AAW53241
ID AAW53241 standard; protein; 354 AA.
XX
AC AAW53241;
XX
DT 03-AUG-1998 (first entry)
XX
DE Homo sapiens vascular endothelial growth factor D (VEGF-D).
XX
KW vascular endothelial growth factor; VEGF-D; angiogenesis; modification;
KW acceleration; wound healing; tissue; organ; transplants;
KW collateral circulation; infarction; arterial stenosis;
KW coronary artery disease; inhibition; cancer; treatment;
KW diabetic retinopathy; lung disorders; blood circulation;
KW gaseous exchange; chronic obstructive airway disease;
KW intestinal malabsorptive syndrome; biopsy; metastatic risk; detection;
KW diagnosis; congestive heart failure.
XX
OS Homo sapiens.

XX
PN WO9807832-A1.
XX
PD 26-FEB-1998.
XX
PF 21-AUG-1997;   97WO-US014696.
XX
PR 23-AUG-1996;   96AU-00001825.
PR 23-AUG-1996;   96US-0023751P.
PR 11-NOV-1996;   96AU-00003554.
PR 14-NOV-1996;   96US-0031097P.
PR 05-FEB-1997;   97AU-00004954.
PR 10-FEB-1997;   97US-0038814P.
PR 19-JUN-1997;   97AU-00007435.
PR 01-JUL-1997;   97US-0051426P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
PI Achen MG, Wilks AF, Stacker SA, Alitalo K;
XX
DR WPI; 1998-179057/16.
DR N-PSDB; AAV20807.
XX
PT New isolated vascular endothelial growth factor-D - used to develop
PT products for use in e.g. modifying angiogenesis or treating lung, heart
PT or intestinal disorders.
XX
PS Claim 16; Page 60-61; 101pp; English.
XX
CC The sequence is that of human lung vascular endothelial growth factor D
CC (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in
CC wound healing, tissue or organ transplantation, or to establish
CC collateral circulation in tissue infarction or arterial stenosis, such as
CC coronary artery disease, and inhibition of angiogenesis in the treatment
CC of cancer or of diabetic retinopathy. It can also be used in the
CC treatment of lung disorders to improve blood circulation in the lung
CC and/or gaseous exchange between the lungs and the blood stream or to
CC improve blood circulation to the heart and O2 gas permeability in cases
CC of cardiac insufficiency, to improve blood flow and gaseous exchange in
CC chronic obstructive airway disease, or to treat malabsorptive syndromes
CC in the intestinal tract. Quantitation of VEGF-D in cancer biopsy
CC specimens may be useful as an indicator of future metastatic risk.
CC Antagonists can be used for treating e.g. conditions such as congestive
CC heart failure, involving accumulations of fluid in the lung resulting
CC from increases in vascular permeability. The products can also be used
CC for detection and diagnosis
XX
SQ Sequence 354 AA;

Query Match   100.0%;   Score 55; DB 2;   Length 354;
Best Local Similarity 100.0%;   Pred. No. 1.8;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
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Db   145 CCNEESLIC 153

RESULT 13
AAB10649
ID AAB10649 standard; protein; 354 AA.
XX
AC AAB10649;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGD protein.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

KW   tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW   venous sore; diabetic ulcer; burns; skin graft growth; VEGD.
XX
OS   Homo sapiens.
XX
PN   WO200037641-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US030503.
XX
PR   22-DEC-1998;   98GB-00028377.
PR   18-MAR-1999;   99US-0124967P.
PR   08-NOV-1999;   99US-0164131P.
XX
PA   (JANC) JANSSEN PHARM NV.
XX
PI   Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI   Dhanaraj SN, Xu J;
XX
DR   WPI; 2000-442669/38.
XX
PT   New vascular endothelial growth factor protein, useful for treating or
PT   preventing diseases associated with inappropriate angiogenesis activity
PT   such as cancer, rheumatoid arthritis, psoriasis and wounds.
XX
PS   Disclosure; Fig 11; 127pp; English.
XX
CC   This invention describes a novel vascular endothelial growth factor-X
CC   (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC   vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC   antidiabetic activity and acts as an angiogenesis and vascularization
CC   regulator. An antisense molecule of the invention is useful for treating
CC   or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC   retinopathy by inhibiting angiogenic activity or inappropriate
CC   vascularization including formation and proliferation of new blood
CC   vessels, growth and development of tissues, tissue regeneration and organ
CC   and tissue repair in a subject. The products of the invention are useful
CC   for preparing medicaments for treating wounds such as dermal ulcers,
CC   pressure sores, venous sores, diabetic ulcers and burns and to promote
CC   skin graft growth, tissue repair, proliferation of new blood vessels,
CC   tissue regeneration and organ repair by promoting angiogenic activity or
CC   vascularization. This sequence represents the human VEGD protein used to
CC   illustrate the method of the invention
XX
SQ   Sequence 354 AA;

Query Match   100.0%; Score 55; DB 3; Length 354;
Best Local Similarity   100.0%; Pred. No. 1.8;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
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Db   145 CCNEESLIC 153

RESULT 14
AAY70750
ID   AAY70750 standard; protein; 354 AA.
XX
AC   AAY70750;
XX
DT   17-AUG-2000 (first entry)
XX
DE   Human prepro-vascular endothelial growth factor D.
XX
KW   Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4;
KW   VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35;
KW   cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis;
KW   neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;
KW   sarcoma; malignancy; VEGF-D; vascular endothelial growth factor D.
XX
OS   Homo sapiens.

XX
PN   WO200021560-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US023525.
XX
PR   09-OCT-1998;   98US-00169079.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI   Alitalo K, Kaipainen A, Valltola R, Jussila L;
XX
DR   WPI; 2000-317850/27.
XX
PT   Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and
PT   sarcomas, involves administering a compound capable of inhibiting binding
PT   of ligand proteins to fms-like tyrosine kinase-1 receptor.
XX
PS   Example 15-17; Page 142-143; 148pp; English.
XX
CC   The patent discloses a method to treat neoplastic disease characterised
CC   by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also
CC   referred as vascular endothelial growth factor receptor-3, VEGFR-3) in
CC   endothelial cells of blood vessels adjacent to malignant neoplasm. The
CC   method involves administering a compound that inhibits binding of a
CC   ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular
CC   endothelial cells. The compound is useful for treating neoplastic disease
CC   such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas
CC   and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used
CC   for manufacturing medicament useful for diagnostic screening, imaging and
CC   treatment of malignancies characterised by Flt4-expressing blood cells.
CC   The Flt4 gene maps to chromosomal region 5q35 and is expressed as 5.8 kb
CC   and 4.5 kb mRNAs which differ in their 3' sequences and are
CC   differentially expressed in HEL and DAMI cell lines. Flt4 belongs to a
CC   subfamily of class III receptor tyrosine kinases (RTKs). It is used as a
CC   target for tumour imaging and anti-tumour therapy. The present sequence
CC   is a human prepro-vascular endothelial growth factor D (VEGF-D), a
CC   specific example of Flt4 binding compound. A recombinantly matured VEGF-D
CC   lacking residues 1-92 and 202-354 retains the ability to activate VEGFR-2
CC   and VEGFR-3 receptors and associate as non-covalently linked dimers
XX
SQ   Sequence 354 AA;

Query Match   100.0%; Score 55; DB 3; Length 354;
Best Local Similarity   100.0%; Pred. No. 1.8;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
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Db   145 CCNEESLIC 153

RESULT 15
AAY70983
ID   AAY70983 standard; protein; 354 AA.
XX
AC   AAY70983;
XX
DT   09-AUG-2000 (first entry)
XX
DE   Human vascular endothelial growth factor (VEGF)-D protein.
XX
KW   vascular endothelial growth factor-D; VEGF; human; re-endothelialisation;
KW   vascular endothelial growth factor receptor; VEGFR; vascular trauma;
KW   blood vessel; cardiovascular surgery; anti-restenosis agent; prevention;
KW   restenosis; stenosis; percutaneous transluminal coronary angioplasty.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
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FT                     /label= Signal_peptide
FT                     /note= "Cleavage results in partially-processed VEGF-D
FT                     protein"
FT       Peptide       22..92
FT                     /label= Amino_terminal_peptide
FT                     /note= "Cleavage results in fully-processed mature VEGF-D
FT                     protein"
FT       Protein       93..201
FT                     /label= Recombinantly_matured VEGF_D protein
FT                     /note= "Processed vascular epithelial growth factor-D"
FT       Peptide       202..354
FT                     /label= Carboxy_terminal_peptide
FT                     /note= "Cleavage results in partially-processed VEGF-D
FT                     protein"
XX
PN   WO20024412-A2.
XX
PD   04-MAY-2000.
XX
PF   26-OCT-1999;   99WO-US024054.
XX
PR   26-OCT-1998;   98US-0105587P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PA   (YLAH/) YLA-HERTTUALA S.
XX
PI   Yla-Herttuala S, Alitalo K, Hiltunen MO, Jeltsch MM, Achen MG;
XX
DR   WPI; 2000-350584/30.
DR   N-PSDB; AAD00340.
XX
PT   Preventing stenosis and restenosis in mammals using vascular endothelial
PT   growth factor proteins or the nucleic acids encoding them.
XX
PS   Disclosure; Page 53-55; 61pp; English.
XX
CC   The present amino acid sequence is the complete human prepro-vascular
CC   endothelial growth factor (VEGF)-D. VEGF-D has the ability to stimulate
CC   re-endothelialisation of an injured blood vessel, without significant
CC   stimulation of smooth muscle cell proliferation. It can bind to and
CC   stimulate VEGFR-2 (vascular endothelial growth factor receptor) and/or
CC   VEGFR-3 phosphorylation in cells that express such receptors. An anti-
CC   restenosis agent comprising either a VEGF-D gene or protein is used in a
CC   method to reduce or prevent restenosis and stenosis of a blood vessel
CC   following vascular trauma e.g., cardiovascular surgery and percutaneous
CC   transluminal coronary angioplasty
XX
SQ   Sequence 354 AA;

Query Match             100.0%;  Score 55;  DB 3;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 1.8;
Matches   9;  Conservative  0;  Mismatches  0;  Indels   0;  Gaps   0;

Qy      1 CCNEESLIC 9
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Db    145 CCNEESLIC 153
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OM protein - protein search, using sw model

Copyright   GenCore version 5.1.6
          (c) 1993 - 2004 Compugen Ltd.

Run on: September 5, 2004, 10:00:15 ; Search time 25.2727 Seconds
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Perfect score: 55
Sequence: 1 CCNEESLIC 9

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Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 1298764

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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                7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	55	100.0	55	73	9	US-09-761-636A-3	Sequence 3, Appli
3	55	100.0	55	96	9	US-09-761-636A-1	Sequence 1, Appli
4	55	100.0	55	109	9	US-09-956-095-3	Sequence 3, Appli
5	55	100.0	55	109	9	US-09-219-345A-1	Sequence 1, Appli
6	55	100.0	55	109	16	US-10-779-731-1	Sequence 1, Appli
7	55	100.0	55	197	12	US-10-352-153-8	Sequence 8, Appli
8	55	100.0	55	280	13	US-10-044-622-1	Sequence 1, Appli
9	55	100.0	55	325	14	US-10-274-953-3	Sequence 3, Appli
10	55	100.0	55	325	14	US-10-161-694-3	Sequence 3, Appli
11	55	100.0	55	354	9	US-09-956-095-2	Sequence 2, Appli
12	55	100.0	55	354	9	US-09-219-345A-11	Sequence 11, Appli
13	55	100.0	55	354	9	US-09-795-006A-119	Sequence 119, App
14	55	100.0	55	354	10	US-09-375-248-6	Sequence 6, Appli
15	55	100.0	55	354	12	US-09-765-534B-22	Sequence 22, Appl
16	55	100.0	55	354	12	US-10-661-740-6	Sequence 6, Appli
17	55	100.0	55	354	14	US-10-262-538-26	Sequence 26, Appl
18	55	100.0	55	354	14	US-10-274-953-5	Sequence 5, Appli
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20	50	90.9	50	9	9	US-09-761-636A-33	Sequence 33, Appl
21	49	89.1	49	9	9	US-09-761-636A-34	Sequence 34, Appl
22	48	87.3	48	354	14	US-10-174-930-1	Sequence 1, Appli
23	48	87.3	48	362	13	US-10-139-876-4	Sequence 4, Appli
24	46	83.6	46	8	8	US-09-761-636A-6	Sequence 6, Appli
25	45	81.8	45	81	13	US-10-086-623-18	Sequence 18, Appl
26	45	81.8	45	81	14	US-10-260-539-18	Sequence 18, Appl
27	45	81.8	45	110	10	US-09-847-524-6	Sequence 6, Appli
28	45	81.8	45	132	9	US-09-795-006A-151	Sequence 151, App
29	45	81.8	45	132	12	US-10-352-153-11	Sequence 11, Appl
30	45	81.8	45	133	9	US-09-852-209A-11	Sequence 11, Appl
31	45	81.8	45	133	12	US-10-439-337A-11	Sequence 11, Appl
32	45	81.8	45	133	12	US-10-303-997B-11	Sequence 11, Appl
33	45	81.8	45	133	14	US-10-352-153-2	Sequence 2, Appli
34	45	81.8	45	133	14	US-10-131-600-11	Sequence 11, Appl
35	45	81.8	45	190	14	US-10-177-485-4	Sequence 4, Appli
36	45	81.8	45	190	14	US-10-155-492-4	Sequence 4, Appli
37	45	81.8	45	321	10	US-09-847-524-4	Sequence 4, Appli
38	45	81.8	45	321	14	US-10-274-953-9	Sequence 9, Appli
39	45	81.8	45	321	14	US-10-161-694-9	Sequence 9, Appli
40	45	81.8	45	358	9	US-09-852-209A-13	Sequence 13, Appl
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42	45	81.8	45	358	12	US-10-439-337A-13	Sequence 13, Appl
43	45	81.8	45	358	12	US-10-303-997B-13	Sequence 13, Appl
44	45	81.8	45	358	13	US-10-139-876-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1
US-09-761-636A-9
; Sequence 9, Application US/09761636A
; Patent No. US2002006521B A1
; GENERAL INFORMATION:
;   APPLICANT: ACHEN, Marc
;   APPLICANT: STACKER, Steven
;   APPLICANT: HUGHES, Richard
;   APPLICANT: CENDRON, Angela
;   TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
;   FILE REFERENCE: 1064/48505 Achen et al
;   CURRENT APPLICATION NUMBER: US/09/761,636A
;   CURRENT FILING DATE: 2001-01-18
;   PRIOR APPLICATION NUMBER: US 60/176,293
;   PRIOR FILING DATE: 2000-01-18
;   PRIOR APPLICATION NUMBER: US 60/204,590
;   PRIOR FILING DATE: 2000-05-16
;   NUMBER OF SEQ ID NOS: 34
;   SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-761-636A-9

Query Match   100.0%; Score 55; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCNEESLIC 9
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Db   1 CCNEESLIC 9

RESULT 2
US-09-761-636A-3
; Sequence 3, Application US/09761636A
; Patent No. US2002006521B A1

; GENERAL INFORMATION:
; , APPLICANT: ACHEN, Marc
; , APPLICANT: STACKER, Steven
; , APPLICANT: HUGHES, Richard
; , APPLICANT: CENDRON, Angela
; , TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; , FILE REFERENCE: 1064/48505 Achen et al
; , CURRENT APPLICATION NUMBER: US 60/176,293
; , CURRENT FILING DATE: 2001-01-18
; , PRIOR APPLICATION NUMBER: US 60/176,293
; , PRIOR FILING DATE: 2000-01-18
; , PRIOR APPLICATION NUMBER: US 60/204,590
; , PRIOR FILING DATE: 2000-05-16
; , NUMBER OF SEQ ID NOS: 34
; , SOFTWARE: PatentIn version 3.0
; , SEQ ID NO 3
; , LENGTH: 73
; , TYPE: PRT
; , ORGANISM: Homo sapiens
; , FEATURE:
; , NAME/KEY: misc feature
; , OTHER INFORMATION: Amino acid residues Val101-Thr173 of VEGF-D

US-09-761-636A-3

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Best Local Similarity   100.0%;   Pred. No. 0.2;
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Qy   1 CCNEESLIC 9
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Db   45 CCNEESLIC 53

RESULT 3
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; Patent No. US20020065218A1
; GENERAL INFORMATION:
; , APPLICANT: ACHEN, Marc
; , APPLICANT: STACKER, Steven
; , APPLICANT: HUGHES, Richard
; , APPLICANT: CENDRON, Angela
; , TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; , FILE REFERENCE: 1064/48505 Achen et al
; , CURRENT APPLICATION NUMBER: US/09761,636A
; , CURRENT FILING DATE: 2001-01-18
; , PRIOR APPLICATION NUMBER: US 60/176,293
; , PRIOR FILING DATE: 2000-01-18
; , PRIOR APPLICATION NUMBER: US 60/204,590
; , PRIOR FILING DATE: 2000-05-16
; , NUMBER OF SEQ ID NOS: 34
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; , SEQ ID NO 1
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; , ORGANISM: Homo sapiens
; , FEATURE:
; , NAME/KEY: misc feature
; , OTHER INFORMATION: Amino acid residues of Val101-Pro196 of VEGF-D

US-09-761-636A-1

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Qy   1 CCNEESLIC 9
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RESULT 4
US-09-956-095-3
; Sequence 3, Application US/09956095

; Patent No. US20020102260A1
; GENERAL INFORMATION:
; , APPLICANT: ACHEN, Marc G.
; , APPLICANT: STACKER, Steven A.
; , TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
; , TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
; , TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
; , TITLE OF INVENTION: VASCULARIZATION OF TISSUE
; , FILE REFERENCE: 1064/48666PC
; , CURRENT APPLICATION NUMBER: US/09/956,095
; , CURRENT FILING DATE: 2001-09-20
; , PRIOR APPLICATION NUMBER: 09/796,714
; , PRIOR FILING DATE: 2001-03-02
; , PRIOR APPLICATION NUMBER: 60/234,196
; , PRIOR FILING DATE: 2000-09-20
; , NUMBER OF SEQ ID NOS: 4
; , SOFTWARE: PatentIn version 3.1
; , SEQ ID NO 3
; , LENGTH: 109
; , TYPE: PRT
; , ORGANISM: Homo sapiens

US-09-956-095-3

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Qy   1 CCNEESLIC 9
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Db   53 CCNEESLIC 61

RESULT 5
US-09-219-345A-1
; Sequence 1, Application US/09219345A
; Patent No. US20020127222A1
; GENERAL INFORMATION:
; , APPLICANT: ACHEN, Marc
; , TITLE OF INVENTION: EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR
; , TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING
; , TITLE OF INVENTION: MELANOMAS
; , FILE REFERENCE: 1064/44385 Marc ACHEN
; , CURRENT APPLICATION NUMBER: US/09/219,345A
; , CURRENT FILING DATE: 1998-12-23
; , PRIOR APPLICATION NUMBER: AU PP 1131
; , PRIOR FILING DATE: 1997-12-24
; , PRIOR APPLICATION NUMBER: US 60/087,392
; , PRIOR FILING DATE: 1998-05-29
; , NUMBER OF SEQ ID NOS: 11
; , SOFTWARE: PatentIn Ver. 2.0
; , SEQ ID NO 1
; , LENGTH: 109
; , TYPE: PRT
; , ORGANISM: Homo sapiens

US-09-219-345A-1

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Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
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; Sequence 1, Application US/10779731
; Publication No. US20040141917A1
; GENERAL INFORMATION:
; , APPLICANT: ACHEN, Marc G.
; , APPLICANT: STACKER, Steve A.
; , TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF

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;    FILE REFERENCE: ACHEN et al-1064-44660
;    CURRENT APPLICATION NUMBER: US/10/779,731
;    CURRENT FILING DATE: 2004-02-18
;    PRIOR APPLICATION NUMBER: US/10/100,037
;    PRIOR FILING DATE: 2002-03-19
;    PRIOR APPLICATION NUMBER: 09/469,186
;    PRIOR FILING DATE: 1999-12-21
;    PRIOR APPLICATION NUMBER: 60/113,254
;    PRIOR FILING DATE: 1998-12-21
;    PRIOR APPLICATION NUMBER: 60/134,556
;    PRIOR FILING DATE: 1999-05-17
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US-10-779-731-1

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Qy          1 CCNEESLIC 9
              |||||||||
Db         53 CCNEESLIC 61

RESULT 7
US-10-352-153-8
; Sequence 8, Application US/10352153
; Publication No. US20030211101A1
; GENERAL INFORMATION:
;    APPLICANT: Wise, Lyn M
;    APPLICANT: Mercer, Andrew A
;    APPLICANT: Savory, Loreen J
;    APPLICANT: Fleming, Stephen B
;    APPLICANT: Stacker, Stephen
;    TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
;    TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
;    TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
;    FILE REFERENCE: Sequence Listing for 09/431,833
;    CURRENT APPLICATION NUMBER: US/10/352,153
;    CURRENT FILING DATE: 2003-01-28
;    PRIOR APPLICATION NUMBER: US/09/431,888A
;    PRIOR FILING DATE: 1999-11-02
;    PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,689
;    PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-02
;    PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,800
;    PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-03
;    NUMBER OF SEQ ID NOS: 11
;    SOFTWARE: PatentIn Ver. 2.0
US-10-352-153-8
;    SEQ ID NO 8
;    LENGTH: 197
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-352-153-8

Query Match             100.0%;  Score 55;  DB 12;  Length 197;
Best Local Similarity   100.0%;  Pred. No. 0.5;
Matches   9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CCNEESLIC 9
              |||||||||
Db         69 CCNEESLIC 77

RESULT 8
US-10-044-622-1
; Sequence 1, Application US/10044622
; Publication No. US20020155538A1
; GENERAL INFORMATION:
;        APPLICANT: Bandman, Olga
;        APPLICANT: Goli, Surya K.
;        APPLICANT: Murry, Lynn E.
;    TITLE OF INVENTION: NOVEL ENDOTHELIAL GROWTH
                         FACTOR
;    NUMBER OF SEQUENCES: 3
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Incyte Pharmaceuticals, Inc.
;       STREET: 3174 Porter Drive
;       CITY: Palo Alto
;       STATE: CA
;       COUNTRY: USA
;       ZIP: 94304
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette
;       COMPUTER: IBM Compatible
;       OPERATING SYSTEM: DOS
;       SOFTWARE: FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/044,622
;       FILING DATE: 09-Jan-2002
;       CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/788,812
;       FILING DATE: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Billings, Lucy J.
;       REGISTRATION NUMBER: 36,749
;       REFERENCE/DOCKET NUMBER: PF-0185 US
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 415-855-0555
;       TELEFAX: 415-845-4166
;    INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 280 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;       IMMEDIATE SOURCE:
;          LIBRARY: LUNGAST01
;          CLONE: 873352
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-622-1

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Best Local Similarity   100.0%;  Pred. No. 0.7;
Matches   9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CCNEESLIC 9
              |||||||||
Db        145 CCNEESLIC 153

RESULT 9
US-10-274-953-3
; Sequence 3, Application US/10274953
; Publication No. US20030114658A1
; GENERAL INFORMATION:
;    APPLICANT: Marc G. ACHEN
;    APPLICANT: Andrew F. WILKS
;    APPLICANT: Steven A. STACKER
;    APPLICANT: Kari ALITALO
;    TITLE OF INVENTION: GROWTH FACTOR
;    NUMBER OF SEQUENCES: 11
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;       STREET: 1200 G Street, NW, Suite 700
;       CITY: Washington
;       STATE: DC
;       COUNTRY: United States of America
;       ZIP: 20005
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/274,953
  FILING DATE: 22-oct-2002
  CLASSIFICATION:
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/296,275
  FILING DATE:
  APPLICATION NUMBER: 08/915,795
  FILING DATE:
ATTORNEY/AGENT INFORMATION:
  NAME: EVANS, Joseph D.
  REGISTRATION NUMBER: 26,269
  REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 628-8800
  TELEFAX: (202) 628-8844
  TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 325 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  HYPOTHETICAL: NO
  ORIGINAL SOURCE:
    TISSUE TYPE: Human Breast
US-10-274-953-3

Query Match   100.0%;   Score 55; DB 14; Length 325;
Best Local Similarity 100.0%;   Pred. No. 0.81;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCNEESLIC 9
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Db   116 CCNEESLIC 124

RESULT 10
US-10-161-694-3
; Sequence 3, Application US/10161694
; Publication No. US20030125537A1
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
;   Andrew F. WILKS
;   Steven A. STACKER
;   Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;   STREET: 1200 G Street, NW, Suite 700
;   CITY: Washington
;   STATE: DC
;   COUNTRY: United States of America
;   ZIP: 20005
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/161,694
;   FILING DATE: 05-Jun-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/296,275
;   FILING DATE: <Unknown>
;   APPLICATION NUMBER: 08/915,795
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:

; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 628-8800
;   TELEFAX: (202) 628-8844
;   TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 325 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
;   TISSUE TYPE: Human Breast
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-161-694-3

Query Match   100.0%;   Score 55; DB 14; Length 325;
Best Local Similarity 100.0%;   Pred. No. 0.81;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCNEESLIC 9
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Db   116 CCNEESLIC 124

RESULT 11
US-09-956-095-2
; Sequence 2, Application US/09956095
; Patent No. US20020102260A1
; GENERAL INFORMATION:
; APPLICANT: STACKER, Steven A.
; APPLICANT: ACHEN, Marc G.
; TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
; TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
; TITLE OF INVENTION: VASCULARIZATION OF TISSUE
; FILE REFERENCE: 1064/48666PC
; CURRENT APPLICATION NUMBER: US/09/956,095
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 09/796,714
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/234,196
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-095-2

Query Match   100.0%;   Score 55; DB 9; Length 354;
Best Local Similarity 100.0%;   Pred. No. 0.88;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCNEESLIC 9
           |||||||||
Db   145 CCNEESLIC 153

RESULT 12
US-09-219-345A-11
; Sequence 11, Application US/09219345A
; Patent No. US20020127222A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; TITLE OF INVENTION: EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING
; TITLE OF INVENTION: MELANOMAS

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;   FILE REFERENCE: 1064/44385 Marc ACHEN
;   CURRENT APPLICATION NUMBER: US/09/219,345A
;   CURRENT FILING DATE: 1998-12-23
;   PRIOR APPLICATION NUMBER: AU PP 1131
;   PRIOR FILING DATE: 1997-12-24
;   PRIOR APPLICATION NUMBER: US 60/087,392
;   PRIOR FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 11
;       LENGTH: 354
;       TYPE: PRT
;       ORGANISM: Homo sapiens
US-09-219-345A-11

Query Match             100.0%;  Score 55;  DB 9;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 0.88;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CCNEESLIC 9
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Db        145 CCNEESLIC 153


RESULT 13
US-09-795-006A-119
;   Sequence 119, Application US/09795006A
;   Patent No. US20020151680A1
;   GENERAL INFORMATION:
;   APPLICANT: Alitalo et al
;   TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
;   TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
;   FILE REFERENCE: 28967/35977B
;   CURRENT APPLICATION NUMBER: US/09/795,006A
;   CURRENT FILING DATE: 2001-02-26
;   PRIOR APPLICATION NUMBER: US 60/205,331
;   PRIOR FILING DATE: 2000-05-18
;   PRIOR APPLICATION NUMBER: US 60/185,205
;   PRIOR FILING DATE: 2000-02-25
;   NUMBER OF SEQ ID NOS: 175
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 119
;       LENGTH: 354
;       TYPE: PRT
;       ORGANISM: Homo sapiens
US-09-795-006A-119

Query Match             100.0%;  Score 55;  DB 9;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 0.88;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CCNEESLIC 9
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Db        145 CCNEESLIC 153


RESULT 14
US-09-375-248-6
;   Sequence 6, Application US/09375248
;   Publication No. US20030026759A1
;   GENERAL INFORMATION:
;   APPLICANT: Ferrell, Robert E.
;   APPLICANT: Alitalo, Kari
;   APPLICANT: Finegold, David N.
;   APPLICANT: Karkkainen, Marika
;   TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
;   TITLE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)
;   FILE REFERENCE: 28967/35255A
;   CURRENT APPLICATION NUMBER: US/09/375,248
;   CURRENT FILING DATE: 1999-08-16
;   EARLIER APPLICATION NUMBER: PCT/US99/06133
;   EARLIER FILING DATE: 1999-03-26
;   NUMBER OF SEQ ID NOS: 28
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;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 6
;       LENGTH: 354
;       TYPE: PRT
;       ORGANISM: Homo sapiens
US-09-375-248-6

Query Match             100.0%;  Score 55;  DB 10;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 0.88;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CCNEESLIC 9
              |||||||||
Db        145 CCNEESLIC 153


RESULT 15
US-09-765-534B-22
;   Sequence 22, Application US/09765534B
;   Publication No. US20040037820A1
;   GENERAL INFORMATION:
;   APPLICANT: Alitalo, Kari
;   APPLICANT: Kaipainen, Arja
;   APPLICANT: Valtola, Reija
;   APPLICANT: Jussila, Lotta
;   TITLE OF INVENTION: Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Thera
;   FILE REFERENCE: 28113/34891
;   CURRENT APPLICATION NUMBER: US/09/765,534B
;   CURRENT FILING DATE: 2001-01-19
;   PRIOR APPLICATION NUMBER: 08/901,710
;   PRIOR FILING DATE: 1997-07-28
;   PRIOR APPLICATION NUMBER: 08/340,011
;   PRIOR FILING DATE: 1994-11-14
;   PRIOR APPLICATION NUMBER: 08/257,754
;   PRIOR FILING DATE: 1994-07-09
;   PRIOR APPLICATION NUMBER: 07/959,951
;   PRIOR FILING DATE: 1992-10-09
;   NUMBER OF SEQ ID NOS: 22
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 22
;       LENGTH: 354
;       TYPE: PRT
;       ORGANISM: Homo sapiens
US-09-765-534B-22

Query Match             100.0%;  Score 55;  DB 12;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 0.88;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CCNEESLIC 9
              |||||||||
Db        145 CCNEESLIC 153


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         Copyright (c) 1993 - 2004  Compugen Ltd.
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(without alignments)
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Title: US-09-761-636A-9
Perfect score: 55
Sequence: 1 CCNEESLIC 9

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Listing first 45 summaries

Database :   Issued Patents AA:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES
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| Result No. | Score | % Query Match | Length | DB | ID | Description |
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| 2 | 55 | 100.0 | 109 | 4 | US-09-469-185-1 | Sequence 1, Appli |
| 3 | 55 | 100.0 | 197 | 4 | US-09-431-888-8 | Sequence 8, Appli |
| 4 | 55 | 100.0 | 325 | 3 | US-08-915-795-3 | Sequence 3, Appli |
| 5 | 55 | 100.0 | 354 | 3 | US-08-915-795-5 | Sequence 5, Appli |
| 6 | 45 | 81.8 | 120 | 6 | 5194596-9 | Patent No. 5194596 |
| 7 | 45 | 81.8 | 120 | 6 | 5219739-9 | Patent No. 5219739 |
| 8 | 45 | 81.8 | 132 | 4 | US-09-125-642C-15 | Sequence 15, Appl |
| 9 | 45 | 81.8 | 132 | 4 | US-09-431-888-11 | Sequence 11, Appl |
| 10 | 45 | 81.8 | 133 | 4 | US-09-431-888-2 | Sequence 2, Appli |
| 11 | 45 | 81.8 | 164 | 6 | 5194596-17 | Patent No. 5194596 |
| 12 | 45 | 81.8 | 164 | 6 | 5219739-17 | Patent No. 5219739 |
| 13 | 45 | 81.8 | 164 | 6 | 5219739-18 | Patent No. 5219739 |
| 14 | 45 | 81.8 | 190 | 6 | 5332671-3 | Patent No. 5332671 |
| 15 | 45 | 81.8 | 321 | 3 | US-08-915-795-9 | Sequence 9, Appli |
| 16 | 45 | 81.8 | 358 | 3 | US-08-915-795-8 | Sequence 8, Appli |
| 17 | 42 | 76.4 | 146 | 3 | US-08-586-039B-33 | Sequence 33, Appl |
| 18 | 42 | 76.4 | 146 | 4 | US-09-699-769-33 | Sequence 33, Appl |
| 19 | 42 | 76.4 | 189 | 1 | US-08-469-427A-15 | Sequence 15, Appl |
| 20 | 42 | 76.4 | 190 | 2 | US-08-569-063C-20 | Sequence 20, Appl |
| 21 | 42 | 76.4 | 190 | 3 | US-08-586-039B-31 | Sequence 31, Appl |
| 22 | 42 | 76.4 | 190 | 3 | US-09-699-769-31 | Sequence 31, Appl |
| 23 | 42 | 76.4 | 214 | 3 | US-08-586-039B-35 | Sequence 35, Appl |
| 24 | 42 | 76.4 | 214 | 4 | US-09-699-769-35 | Sequence 35, Appl |
| 25 | 41 | 74.5 | 12 | 3 | US-08-742-243-43 | Sequence 43, Appl |
| 26 | 41 | 74.5 | 12 | 3 | US-08-742-243-44 | Sequence 44, Appl |
| 27 | 41 | 74.5 | 65 | 4 | US-09-244-583-12 | Sequence 12, Appl |
| 28 | 41 | 74.5 | 109 | 3 | US-08-691-794-3 | Sequence 3, Appli |
| 29 | 41 | 74.5 | 110 | 4 | US-09-392-932-11 | Sequence 11, Appl |
| 30 | 41 | 74.5 | 110 | 4 | US-09-574-708A-11 | Sequence 11, Appl |
| 31 | 41 | 74.5 | 110 | 4 | US-09-822-270-17 | Sequence 17, Appl |
| 32 | 41 | 74.5 | 110 | 4 | US-09-392-931-10 | Sequence 10, Appl |
| 33 | 41 | 74.5 | 110 | 4 | US-09-392-931-11 | Sequence 11, Appl |
| 34 | 41 | 74.5 | 121 | 6 | 5194596-19 | Patent No. 5194596 |
| 35 | 41 | 74.5 | 121 | 6 | 5219739-20 | Patent No. 5219739 |
| 36 | 41 | 74.5 | 136 | 4 | US-09-037-983C-15 | Sequence 15, Appl |
| 37 | 41 | 74.5 | 137 | 4 | US-09-037-983C-17 | Sequence 17, Appl |
| 38 | 41 | 74.5 | 138 | 4 | US-09-037-983C-16 | Sequence 16, Appl |
| 39 | 41 | 74.5 | 141 | 4 | US-09-519-476-2 | Sequence 2, Appli |
| 40 | 41 | 74.5 | 145 | 3 | US-08-784-551C-2 | Sequence 2, Appli |
| 41 | 41 | 74.5 | 145 | 4 | US-09-392-932-2 | Sequence 2, Appli |
| 42 | 41 | 74.5 | 145 | 4 | US-09-574-708A-4 | Sequence 4, Appli |
| 43 | 41 | 74.5 | 145 | 4 | US-09-037-983C-2 | Sequence 2, Appli |
| 44 | 41 | 74.5 | 145 | 4 | US-09-428-909A-2 | Sequence 2, Appli |
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                    ALIGNMENTS

RESULT 1
US-09-469-186-1
; Sequence 1, Application US/09469186
; Patent No. 6383484
; GENERAL INFORMATION:
;  APPLICANT: ACHEN, Marc G.
;  APPLICANT: STACKER, Steve A.
;  TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
;  FILE REFERENCE: ACHEN et al-1064-44660
;  CURRENT APPLICATION NUMBER: US/09/469,186
;  CURRENT FILING DATE: 1999-12-21
;  EARLIER APPLICATION NUMBER: 60/113,254
;  EARLIER FILING DATE: 1998-12-21
;  EARLIER APPLICATION NUMBER: 60/134,556
;  EARLIER FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;  LENGTH: 109
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-469-186-1

Query Match             100.0%;  Score 55;  DB 4;  Length 109;
Best Local Similarity   100.0%;  Pred. No. 0.15;
Matches    9; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy      1 CCNEESLIC 9
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Db     53 CCNEESLIC 61

RESULT 2
US-09-469-185-1
; Sequence 1, Application US/09469185
; Patent No. 6531185
; GENERAL INFORMATION:
;  APPLICANT: ACHEN, Marc G.
;  APPLICANT: STACKER, Steve A.
;  TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
;  FILE REFERENCE: ACHEN et al-1064-44660
;  CURRENT APPLICATION NUMBER: US/09/469,185
;  CURRENT FILING DATE: 1999-12-21
;  EARLIER APPLICATION NUMBER: 60/113,254
;  EARLIER FILING DATE: 1998-12-21
;  EARLIER APPLICATION NUMBER: 60/134,556
;  EARLIER FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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;    LENGTH: 109
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-469-185-1

Query Match             100.0%;   Score 55;   DB 4;   Length 109;
Best Local Similarity   100.0%;   Pred. No. 0.15;
Matches    9;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy          1 CCNEESLIC 9
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Db         53 CCNEESLIC 61


RESULT 3
US-09-431-888-8
;  Sequence 8, Application US/09431888A
;  Patent No. 6541008
;  GENERAL INFORMATION:
;    APPLICANT: Wise, Lyn M
;    APPLICANT: Mercer, Andrew A
;    APPLICANT: Savory, Loreen J
;    APPLICANT: Fleming, Stephen B
;    APPLICANT: Stacker, Stephen
;    TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
;    TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
;    TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
;    FILE REFERENCE: Sequence Listing for 09/431,833
;  Patent No. 6541008
;    CURRENT APPLICATION NUMBER: US/09/431,888A
;    CURRENT FILING DATE: 1999-11-02
;    EARLIER APPLICATION NUMBER: 60/106,689
;    EARLIER FILING DATE: 1998-11-02
;    EARLIER APPLICATION NUMBER: 60/106,800
;    EARLIER FILING DATE: 1998-11-03
;    NUMBER OF SEQ ID NOS: 11
;    SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 8
;    LENGTH: 197
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-431-888-8

Query Match             100.0%;   Score 55;   DB 4;   Length 197;
Best Local Similarity   100.0%;   Pred. No. 0.25;
Matches    9;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy          1 CCNEESLIC 9
              |||||||||
Db         69 CCNEESLIC 77


RESULT 4
US-08-915-795-3
;  Sequence 3, Application US/08915795
;  Patent No. 6235713
;  GENERAL INFORMATION:
;    APPLICANT: Marc G. ACHEN
;    APPLICANT: Andrew F. WILKS
;    APPLICANT: Steven A. STACKER
;    APPLICANT: Kari ALITALO
;    TITLE OF INVENTION: GROWTH FACTOR
;    NUMBER OF SEQUENCES: 11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;      STREET: 1200 G Street, NW, Suite 700
;      CITY: Washington
;      STATE: DC
;      COUNTRY: United States of America
;      ZIP: 20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
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;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/915,795
;      FILING DATE:
;      CLASSIFICATION: 536
;    ATTORNEY/AGENT INFORMATION:
;      NAME: EVANS, Joseph D.
;      REGISTRATION NUMBER: 26,269
;      REFERENCE/DOCKET NUMBER: 1064/42983
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-8800
;      TELEFAX:    (202) 628-8844
;      TELEX: N/A
;  INFORMATION FOR SEQ ID NO: 3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 325 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: protein
;    HYPOTHETICAL: NO
;    ORIGINAL SOURCE:
;      TISSUE TYPE: Human Breast
US-08-915-795-3

Query Match             100.0%;   Score 55;   DB 3;   Length 325;
Best Local Similarity   100.0%;   Pred. No. 0.4;
Matches    9;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy          1 CCNEESLIC 9
              |||||||||
Db        116 CCNEESLIC 124


RESULT 5
US-08-915-795-5
;  Sequence 5, Application US/08915795
;  Patent No. 6235713
;  GENERAL INFORMATION:
;    APPLICANT: Marc G. ACHEN
;    APPLICANT: Andrew F. WILKS
;    APPLICANT: Steven A. STACKER
;    APPLICANT: Kari ALITALO
;    TITLE OF INVENTION: GROWTH FACTOR
;    NUMBER OF SEQUENCES: 11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;      STREET: 1200 G Street, NW, Suite 700
;      CITY: Washington
;      STATE: DC
;      COUNTRY: United States of America
;      ZIP: 20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/915,795
;      FILING DATE:
;      CLASSIFICATION: 536
;    ATTORNEY/AGENT INFORMATION:
;      NAME: EVANS, Joseph D.
;      REGISTRATION NUMBER: 26,269
;      REFERENCE/DOCKET NUMBER: 1064/42983
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-8800
;      TELEFAX:    (202) 628-8844
;      TELEX: N/A
;  INFORMATION FOR SEQ ID NO: 5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 354 amino acids
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;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     HYPOTHETICAL: NO
;     ORIGINAL SOURCE:
;       TISSUE TYPE: Human Lung
US-08-915-795-5

Query Match             100.0%;  Score 55;  DB 3;  Length 354;
Best Local Similarity   100.0%;  Pred. No. 0.43;
Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCNEESLIC 9
           |||||||||
Db     145 CCNEESLIC 153


RESULT 6
5194596-9
;Patent No. 5194596
;     APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES, JOHN
;C.;MITCHELL, RICHARD L.
;     TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
;GROWTH FACTOR
;     NUMBER OF SEQUENCES: 32
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/07/450,883
;       FILING DATE: 14-DEC-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 387,545
;       FILING DATE: 27-JUL-1989
;SEQ ID NO:9:
;     LENGTH: 120
5194596-9

Query Match             81.8%;  Score 45;  DB 6;  Length 120;
Best Local Similarity   77.8%;  Pred. No. 4.9;
Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCNEESLIC 9
           |||:|||||
Db      59 CCNDESLEC 67


RESULT 7
5219739-9
;Patent No. 5219739
;     APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES,
;JOHN C.;MITCHELL, RICHARD L.
;     TITLE OF INVENTION: DNA SEQUENCES ENCODING BVEGF120 AND
;HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
;VAASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVEGF120 AND HVEGF121
;     NUMBER OF SEQUENCES: 40
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/07/559,041
;       FILING DATE: 27-JUL-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 450,883
;       FILING DATE: 14-DEC-1989
;       APPLICATION NUMBER: 387,545
;       FILING DATE: 27-JUL-1989
;SEQ ID NO:9:
;     LENGTH: 120
5219739-9

Query Match             81.8%;  Score 45;  DB 6;  Length 120;
Best Local Similarity   77.8%;  Pred. No. 4.9;
Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCNEESLIC 9
           |||:|||||
Db      59 CCNDESLEC 67
```

```
RESULT 8
US-09-125-642C-15
; Sequence 15, Application US/09125642C
; Patent No. 6365393
;     GENERAL INFORMATION:
;       APPLICANT: BAYER AG
;       TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
;                           Their Production and Their Use in Vaccines
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE: Bayer Corporation
;         STREET: 100 Bayer Road
;         CITY: Pittsburgh
;         STATE: Pennsylvania
;         COUNTRY: U.S.A.
;         ZIP: 15205-9741
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: PC-DOS/MS-DOS
;         SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/09/125,642C
;         FILING DATE: 20-Aug-1998
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: PCT/EP97/00729,
;         FILING DATE: 17-Feb-97
;     INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 132 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       ORIGINAL SOURCE:
;         ORGANISM: Parapox ovis
;         STRAIN: D1701 VEGF- Protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-125-642C-15

Query Match             81.8%;  Score 45;  DB 4;  Length 132;
Best Local Similarity   77.8%;  Pred. No. 5.3;
Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCNEESLIC 9
           |||:|||||
Db      69 CCNDESLEC 77


RESULT 9
US-09-431-888-11
; Sequence 11, Application US/09431888A
; Patent No. 6541008
;     GENERAL INFORMATION:
;       APPLICANT: Wise, Lyn M
;       APPLICANT: Mercer, Andrew A
;       APPLICANT: Savory, Loreen J
;       APPLICANT: Fleming, Stephen B
;       APPLICANT: Stacker, Stephen
;       TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
;       TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
;       TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
;       FILE REFERENCE: Sequence Listing for 09/431,833
; Patent No. 6541008
;       CURRENT APPLICATION NUMBER: US/09/431,888A
;       CURRENT FILING DATE: 1999-11-02
;       EARLIER APPLICATION NUMBER: 60/106,689
;       EARLIER FILING DATE: 1998-11-02
;       EARLIER APPLICATION NUMBER: 60/106,800
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; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;     LENGTH: 132
;     TYPE: PRT
;     ORGANISM: Orf virus
US-09-431-888-11

Query Match          81.8%;  Score 45;  DB 4;  Length 132;
Best Local Similarity  77.8%;  Pred. No. 5.3;
Matches   7; Conservative   1; Mismatches   1; Indels   1; Gaps   0;

Qy     1 CCNEESLIC 9
           |||:|||||
Db    69 CCNDESLEC 77


RESULT 10
US-09-431-888-2
; Sequence 2, Application US/09431888A
; Patent No. 6541008
; GENERAL INFORMATION:
; APPLICANT: Wise, Lyn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stacker, Stephen
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
; TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
; TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence listing for 09/431,833
; Patent No. 6541008
; CURRENT APPLICATION NUMBER: US/09/431,888A
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/106,689
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/106,800
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;     LENGTH: 133
;     TYPE: PRT
;     ORGANISM: Orf virus
US-09-431-888-2

Query Match          81.8%;  Score 45;  DB 4;  Length 133;
Best Local Similarity  77.8%;  Pred. No. 5.3;
Matches   7; Conservative   1; Mismatches   1; Indels   1; Gaps   0;

Qy     1 CCNEESLIC 9
           |||:|||||
Db    70 CCNDESLEC 78


RESULT 11
5194596-17
;Patent No. 5194596
;     APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES, JOHN
;C.;MITCHELL, RICHARD L.
;     TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
;GROWTH FACTOR
;     NUMBER OF SEQUENCES: 32
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/07/450,883
;       FILING DATE: 14-DEC-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 387,545
;       FILING DATE: 27-JUL-1989
;SEQ ID NO:17:
;     LENGTH: 164
5194596-17
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Query Match          81.8%;  Score 45;  DB 6;  Length 164;
Best Local Similarity  77.8%;  Pred. No. 6.4;
Matches   7; Conservative   1; Mismatches   1; Indels   1; Gaps   0;

Qy     1 CCNEESLIC 9
           |||:|||||
Db    59 CCNDESLEC 67


RESULT 12
5219739-17
;Patent No. 5219739
;     APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES,
;JOHN C.;MITCHELL, RICHARD L.
;     TITLE OF INVENTION: DNA SEQUENCES ENCODING BVEGF120 AND
;HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
;VAASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVEGF120 AND HVEGF121
;     NUMBER OF SEQUENCES: 40
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/07/559,041
;       FILING DATE: 27-JUL-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 450,883
;       FILING DATE: 14-DEC-1989
;       APPLICATION NUMBER: 387,545
;       FILING DATE: 27-JUL-1989
;SEQ ID NO:17:
;     LENGTH: 164
5219739-17

Query Match          81.8%;  Score 45;  DB 6;  Length 164;
Best Local Similarity  77.8%;  Pred. No. 6.4;
Matches   7; Conservative   1; Mismatches   1; Indels   1; Gaps   0;

Qy     1 CCNEESLIC 9
           |||:|||||
Db    59 CCNDESLEC 67


RESULT 13
5219739-18
;Patent No. 5219739
;     APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES,
;JOHN C.;MITCHELL, RICHARD L.
;     TITLE OF INVENTION: DNA SEQUENCES ENCODING BVEGF120 AND
;HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
;VAASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVEGF120 AND HVEGF121
;     NUMBER OF SEQUENCES: 40
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/07/559,041
;       FILING DATE: 27-JUL-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 450,883
;       FILING DATE: 14-DEC-1989
;       APPLICATION NUMBER: 387,545
;       FILING DATE: 27-JUL-1989
;SEQ ID NO:18:
;     LENGTH: 164
5219739-18

Query Match          81.8%;  Score 45;  DB 6;  Length 164;
Best Local Similarity  77.8%;  Pred. No. 6.4;
Matches   7; Conservative   1; Mismatches   1; Indels   1; Gaps   0;

Qy     1 CCNEESLIC 9
           |||:|||||
Db    59 CCNDESLEC 67


RESULT 14
5332671-3
;Patent No. 5332671
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Matches   6; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   1 CCNEESLIC 9
          |||| :|
Db   145 CCNEEGVMC 153

Search completed: September 5, 2004, 10:21:58
Job time : 8 secs

; APPLICANT: FERRARA, NAPOLEONE;LEUNG, DAVID W.H.
; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
;GROWTH FACTOR AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/389,722
;   FILING DATE: 04-AUG-1989
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 369,424
;   FILING DATE: 21-JUN-1989
;   APPLICATION NUMBER: 351,117
;   FILING DATE: 12-MAY-1989
;SEQ ID NO:3:
;   LENGTH: 190
5332671-3

Query Match   81.8%; Score 45; DB 6; Length 190;
Best Local Similarity   77.8%; Pred. No. 7.3;
Matches   7; Conservative   1; Mismatches   1; Indels   1; Gaps   0;

Qy   1 CCNEESLIC 9
          |||:|||
Db   85 CCNDESLEC 93

RESULT 15
US-08-915-795-9
; Sequence 9, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
;   APPLICANT: Marc G. ACHEN
;   APPLICANT: Andrew F. WILKS
;   APPLICANT: Steven A. STACKER
;   APPLICANT: Kari ALITALO
;   TITLE OF INVENTION: GROWTH FACTOR
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;   STREET: 1200 G Street, NW, Suite 700
;   CITY: Washington
;   STATE: DC
;   COUNTRY: United States of America
;   ZIP: 20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/915,795
;   FILING DATE:
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: EVANS, Joseph D.
;   REGISTRATION NUMBER: 26,269
;   REFERENCE/DOCKET NUMBER: 1064/42983
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 628-8800
;   TELEFAX: (202) 628-8844
;   TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 321 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   ORIGINAL SOURCE:
;   TISSUE TYPE: Mouse Lung
US-08-915-795-9

Query Match   81.8%; Score 45; DB 3; Length 321;
Best Local Similarity   66.7%; Pred. No. 12;

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